

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:05:26 / Search time 1878 Seconds  
(without alignments)  
5363.528 Million cell updates/sec

Title: US-10-089-473a-2

Perfect score: 213

Sequence: 1 ggaagaagatgctgctgctg.....ccagaatccctccatgcc 213

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_da.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	222	5	AY005480
2	209.8	98.5	1989	5	AF051789
3	206.6	97.0	234	5	AY259516
4	201.8	94.7	712	5	AY204249
5	201.8	94.7	1977	5	AY204245
6	201.8	94.7	2045	5	AF345931
7	198.6	93.2	270	5	AF551929
8	198.6	93.2	318	5	AF054626
9	198.6	93.2	972	5	AF367868
10	198.6	93.2	1558	6	AK005242
11	198.6	93.2	1558	6	AK005242
12	197	92.5	222	6	AF367867
13	197	92.5	917	5	AF051788
14	195.4	91.7	1983	5	AB059572
15	193.8	91.0	222	6	E39840
16	193.8	91.0	222	6	AR287876
17	193.8	91.0	2017	5	TGTRICRA
18	193.8	89.5	2018	5	AF212305
19	190.6	89.5	2018	5	AF212305

20	190.6	89.5	2029	6	BD244771
21	190.6	89.5	2029	6	AR489412
22	190.6	89.5	2031	5	AB078804
23	189	88.7	2029	5	AB078806
24	185.8	87.2	2102	6	AX28621
25	184.2	86.5	1205	5	AY258153
26	182.6	85.7	712	5	AY204248
27	182.6	85.7	1992	5	AY204244
28	179.4	84.2	1929	5	AF051790
29	177.8	83.5	1475	5	TWETDIS
30	176.2	82.7	222	5	AF1917762
31	176.2	82.7	1482	5	TWETMET
32	176.2	82.7	2028	5	TRIMUT
33	174.8	82.1	2009	5	AB059571
34	173.2	81.3	1455	5	AY644231
35	173	81.2	540	5	AF055337
36	173	81.2	1999	5	AY037808
37	171.4	80.5	213	5	AF131345
38	171.4	80.5	1471	5	AF162086
39	171.4	80.5	1476	5	AAJ3283
40	171.4	80.5	1863	5	AF117636
41	171.4	80.5	1863	5	AF117637
42	168.2	79.0	1446	5	AY67902
43	167	78.4	911	6	AR43807
44	166.8	78.3	1467	5	AF071905
45	166	77.9	2001	5	AB052155

## ALIGNMENTS

RESULT 1  
LOCUS AY005480 222 bp mRNA linear VRT 23-AUG-2000  
DEFINITION Gloydius halys saxatillin mRNA, partial cds.  
ACCESSION AY005480  
VERSION AY005480.1 GI:9945027  
KEYWORDS  
SOURCE Gloydius halys (halys viper)  
ORGANISM Gloydius halys  
REFERENCE 1 (bases 1 to 222)  
AUTHORS Chung,K.-H., Koh,Y.-S., Hong,S.-Y. and Kim,D.-S.  
TITLE Snake venom disintegrin, saxatillin cDNA  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 222)  
AUTHORS Chung,K.-H., Koh,Y.-S., Hong,S.-Y. and Kim,D.-S.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-2000) Biochemistry, Yonsei Univ., Seodaemun Ku  
Shincheon Dong 134, Seoul 120-749, Korea  
FEATURES  
source  
1..222  
/organism="Gloydius halys"  
/mol\_type="mRNA"  
/db\_xref="taxon:8714"  
/tissue\_type="venom gland"  
CDS  
1..222  
/note="disintegrin"  
/codon\_start=1  
/product="saxatillin"  
/protein\_id="AAG01882.1"  
/db\_xref="GI:9945028"  
/translation="EAGGECDCGAPRNCDAATCKAPGACAGLCCDQCFMKKEG  
TICRMARGDDMDVYCNGISAGCFRPFPA"  
ORIGIN  
Query Match 100.0%; Score 213; DB 5; Length 222;  
Best Local Similarity 100.0%; Pred. No. 4,3e-57;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTGTGCGGAGTGGCAACTGTGTA 60

Db 7 GGAGAGAGATGATGCTGGCGCTCTCTCAATCCGTCGATGCTGCAACCTGTAAA 66  
Qy 61 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 120  
Db 67 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 126  
Qy 121 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 180  
Db 127 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 186  
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
Db 187 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 219

RESULT 2  
LOCUS AF051789 1989 bp mRNA linear VRT 08-NOV-1999  
DEFINITION Gloydius halys metalloprotease (Mt-d) mRNA, complete cds.  
ACCESSION AF051789  
VERSION AF051789.1 GI:4106004  
KEYWORDS  
SOURCE Gloydius halys (hals viper)  
ORGANISM Gloydius halys  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Gloydius.  
REFERENCE  
AUTHORS Jeon, O.H. and Kim, D.S.  
TITLE Molecular cloning and functional characterization of a snake venom metalloprotease  
JOURNAL Eur J Biochem. 263 (2), 526-533 (1999)  
MEDLINE 99337693  
PubMed 10406963  
REFERENCE 2 (bases 1 to 1989)  
AUTHORS Jeon, O.H. and Kim, D.S.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAR-1998) Biochemistry, Yonsei University, 134  
Shincheon-dong Seodaemun-Gu, Seoul 120-749, Korea

FEATURES  
source  
1..1989  
/organism="Gloydius halys"  
/mol\_type="mRNA"  
/strain="brevicaudus"  
/db\_xref="taxon:8714"  
/tissue\_type="venom"  
1..1989  
/gene="Mt-d"  
51..1499  
/gene="Mt-d"  
/codon\_start=1  
/product="metalloprotease"  
/protein\_id="AA02654.1"  
/db\_xref="GI:4106005"  
/translation="MTDVLVTICLAAPFYQSGSMILESGANDVEVYVQKYPALPK  
GAVPKEDADQYEFKNGEPEVLAHLKKNKLFKDYSETHYSDEGKITTNPVEDE  
CYVGHILNDADSTASISACNGKGFHKEQEMYLEPLKIDSFAVAAYENVEKE  
DEAPMGCVTQTNKSDPFIKASQLVYTAEOQRPORYELVYVADAGMTTKDSND  
TITPMVELVANNINEFYSRLNVRYSLLELWISMODLINVOSAADLTLEAFGMBRD  
LNRISNDNADLTITDIDGNTIGLAHVGMDPKYSGIVQDSAINLILVATMAE  
LGNHGNHDNOCCHCGSNSSVMGDYLRVGSYSPFCNENREYVYTTIDNPCCIANE  
PLRDTVSTPVSGBELLFAGVECDGAPANPCDAATCKLRPGAQCAEGLCCQCCRM  
KEGTCRMARDMDYDVCNGISACFPNPFHA"

ORIGIN  
Query Match 98.5%; Score 209.8; DB 5; Length 1989;  
Best Local Similarity 99.1%; Pred. No. 4,5e-56;  
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGAGATGATGCTGGCGCTCTCTCAATCCGTCGATGCTGCAACCTGTAAA 60  
Db 1284 GGAGATTGAATGATGCTGGCGCTCTCTCAATCCGTCGATGCTGCAACCTGTAAA 1343

Qy 61 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 120  
Db 1344 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 1403  
Qy 121 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 180  
Db 1404 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 1463  
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
Db 1464 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 1496

RESULT 3  
LOCUS AY259516 234 bp mRNA linear VRT 03-APR-2003  
DEFINITION Bothrops alternatus disintegrin mRNA, partial cds.  
ACCESSION AY259516  
VERSION AY259516.1 GI:29501767  
KEYWORDS  
SOURCE Bothrops alternatus  
ORGANISM Bothrops alternatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.  
REFERENCE  
AUTHORS Ramos, O.H.P. and Selistre-de-Araujo, H.S.  
TITLE Cloning and expression of disintegrins from Bothrops alternatus  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 234)  
AUTHORS Ramos, O.H.P. and Selistre-de-Araujo, H.S.  
TITLE Direct Submission  
JOURNAL Submitted (20-MAR-2003) Depto. de Ciencias Fisiologicas,  
Universidade Federal de Sao Carlos, Rodovia Washington Luis  
(SP-310), Km 235, Sao Carlos, Sao Paulo 13565-905, Brazil

FEATURES  
source  
1..234  
/organism="Bothrops alternatus"  
/mol\_type="mRNA"  
/db\_xref="taxon:64174"  
1..234  
/note="Disin-01; belongs to the RGD family of  
disintegrins"  
/codon\_start=1  
/product="disintegrin"  
/protein\_id="AA075107.1"  
/db\_xref="GI:29501768"  
/translation="NELLEAGBECDGTPNPPCCDAATCKLRPGAQCAEGLCCQCCRM  
KEGTCRMARDMDYDVCNGISACFPNPFHA"

ORIGIN  
Query Match 97.0%; Score 206.6; DB 5; Length 234;  
Best Local Similarity 98.1%; Pred. No. 4,8e-55;  
Matches 209; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAGAGATGATGCTGGCGCTCTCTCAATCCGTCGATGCTGCAACCTGTAAA 60  
Db 19 GGAGAGAGATGATGCTGGCGCTCTCTCAATCCGTCGATGCTGCAACCTGTAAA 78  
Qy 61 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 120  
Db 79 CTGAGACCAAGGGCCGACGTGTGACAGAGAGACTGTGTGTACCGCTGACATTTATGAAA 138  
Qy 121 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 180  
Db 139 GAAGGAACAATATGCGGATGCGAAGGGGTATGATGATGATTAATGCAATGGCATA 198  
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
Db 199 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 231

RESULT 4  
LOCUS AY204249 712 bp mRNA linear VRT 01-JUN-2003  
DEFINITION Gloydius ussuriensis disintegrin mRNA, partial cds.  
ACCESSION AY204249  
VERSION AY204249.1 GI:31322310  
KEYWORDS  
SOURCE Gloydius ussuriensis  
ORGANISM Gloydius ussuriensis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Gloydius.  
1 (bases 1 to 712)  
Sun, D.-J. and Yang, T.-S.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (17-DEC-2002) Biochemistry Lab, Frontier Medical Science  
JOURNAL Institute, Jilin University, No. 13 Xinmin Street, Changchun,  
Jilin 130021, China  
FEATURES  
source Location/Qualifiers  
1..712  
/organism="Gloydius ussuriensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:35671"  
/tissue\_type="snake venom gland"  
/country="China: northeast area"  
1..222  
/codon\_start=1  
/product="disintegrin"  
/protein\_id="AAP20644.1"  
/db\_xref="GI:31322311"  
/translation="EAGEECDCDSRPNPCDDAATCKLRPGAOCAGLCCGCRPMKRG  
TVCRIRAGDDMDYCNGISAGCPNPFHA"  
ORIGIN  
Query Match 94.7%; Score 201.8; DB 5; Length 712;  
Best Local Similarity 96.7%; Pred. No. 1.7e-53;  
Matches 206; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 GGAGAGAAATGTGACTGTGCGCTCTCCGCAATCCGTCGATGCTGCAACCTGTAA 60  
DB 7 GGAGAGAAATGTGACTGTGCGCTCTCCGCAATCCGTCGATGCTGCAACCTGTAA 66  
QY 61 CTGAGACCAAGGGCGGCGAGTGTGCAAGAGACTGTGTTGTGACCCAGTGCAATTTATGAA 120  
DB 67 CTGAGACCAAGGGCGGCGAGTGTGCAAGAGACTGTGTTGTGACCCAGTTTATGAA 126  
QY 121 GAAGGAACAATATGCGCGATGGCAAGGGGTGATGATGATGATCTGCAATGGCATA 180  
DB 127 GAAGGAACAATATGCGCGATGGCAAGGGGTGATGATGATGATCTGCAATGGCATA 186  
QY 181 TCTGCTGGCTGTCCCAAGAAATCCCTTCATGCC 213  
DB 187 TCTGCTGGCTGTCCCAAGAAATCCCTTCATGCC 219

RESULT 5  
LOCUS AY204245 1977 bp mRNA linear VRT 01-JUN-2003  
DEFINITION Gloydius ussuriensis metalloproteinase/disintegrin ussuriin  
precursor, mRNA, partial cds.  
ACCESSION AY204245  
VERSION AY204245.1 GI:31322302  
KEYWORDS  
SOURCE Gloydius ussuriensis  
ORGANISM Gloydius ussuriensis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Gloydius.  
1 (bases 1 to 1977)  
Sun, D.-J. and Yang, T.-S.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (17-DEC-2002) Biochemistry Lab, Frontier Medical Science  
JOURNAL Institute, Jilin University, No. 13 Xinmin Street, Changchun,  
Jilin 130021, China  
FEATURES  
source Location/Qualifiers  
1..1977  
/organism="Gloydius ussuriensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:35671"  
/tissue\_type="snake venom gland"  
/country="China: northeast area"  
51..1487  
/codon\_start=1  
/product="metalloproteinase/disintegrin ussuriin precursor"  
/protein\_id="AAP20640.1"  
/db\_xref="GI:31322303"  
/translation="MIOVLITTCIAAPFYCCSSITLESNNNDYEIVPRKVTALPK  
GAVPRIEDTQYELKVGEPVHLKNGKLSKDYSETHYSPGKRTTPVEDH  
CYHRIQNDADSTASISACNGKSHFLQGEMLIEBKLSDSBAHAFYEHLEKE  
DEDPRMCGVTEINMESYEPKIKASPLVVTYQRYVELVYVADHRYVWNGNLIIIRT  
WYVEIENITNEYCRMNIHVALVGLVLSNEDKIIIVQSSADVTLDLFTWGEIDLKR  
KSHDNAOLTPDFDPTIGLAVYGTMGDPKRSRTGVQDFPINLVAVTAAHETGN  
LGMNDENYCSGCFRACIMSPVISPQSKLSYCSYHYMTYINRYNPOCILTNPRT  
DIVSRVSGNHELLENGECCDDSPNPPCDDAATCKLRPGAOCAGLCCGCRPMKRG  
TVCRIRAGDDMDYCNGISAGCPNPFHA"  
ORIGIN  
Query Match 94.7%; Score 201.8; DB 5; Length 1977;  
Best Local Similarity 96.7%; Pred. No. 1.6e-53;  
Matches 206; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 GGAGAGAAATGTGACTGTGCGCTCTCCGCAATCCGTCGATGCTGCAACCTGTAA 60  
DB 1272 GGAGAGAAATGTGACTGTGCGCTCTCCGCAATCCGTCGATGCTGCAACCTGTAA 1331  
QY 61 CTGAGACCAAGGGCGGCGAGTGTGCAAGAGACTGTGTTGTGACCCAGTGCAATTTATGAA 120  
DB 1332 CTGAGACCAAGGGCGGCGAGTGTGCAAGAGACTGTGTTGTGACCCAGTGCAATTTATGAA 1391  
QY 121 GAAGGAACAATATGCGCGATGGCAAGGGGTGATGATGATGATCTGCAATGGCATA 180  
DB 1392 GAAGGAACAATATGCGCGATGGCAAGGGGTGATGATGATGATCTGCAATGGCATA 1451  
QY 181 TCTGCTGGCTGTCCCAAGAAATCCCTTCATGCC 213  
DB 1452 TCTGCTGGCTGTCCCAAGAAATCCCTTCATGCC 1484

RESULT 6  
LOCUS AF345931 2045 bp mRNA linear VRT 04-MAR-2001  
DEFINITION Bothrops jararaca bothrostatin precursor, mRNA, complete cds.  
ACCESSION AF345931  
VERSION AF345931.1 GI:13194759  
KEYWORDS  
SOURCE Bothrops jararaca  
ORGANISM Bothrops jararaca  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.  
1 (bases 1 to 2045)  
Silva, C.A., Martins de Camargo, A.C. and de Toledo Serrano, S.M.  
REFERENCE  
AUTHORS Molecular cloning of a cDNA encoding bothrostatin, a precursor of a  
RGD containing disintegrin from Bothrops jararaca venom  
JOURNAL Unpublished  
TITLE 2 (bases 1 to 2045)  
AUTHORS Silva, C.A., Martins de Camargo, A.C. and de Toledo Serrano, S.M.  
JOURNAL Direct Submission  
TITLE Submitted (05-FEB-2001) Bioquímica e Biofísica, Instituto Butantan,  
Av. Vital Brasil 1500, Sao Paulo 05503-900, Brazil  
FEATURES  
source Location/Qualifiers  
1..2045  
/organism="Bothrops jararaca"  
/mol\_type="mRNA"  
/db\_xref="taxon:8724"  
/note="isolated from venom"

CDS

86..1519  
/note="RGD-containing disintegrin"  
/codon\_start=1  
/product="bothrostatin precursor"  
/protein\_id="AAK15542.1"  
/db\_xref="GI:13194760"

ORIGIN

Query Match 94.7%; Score 201.8; DB 5; Length 2045;  
Best Local Similarity 96.7%; Pred. No. 1.6e-53;  
Matches 206; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGTGACTGTGGCGCTCTCGCAATCCGTCCTGGATGCTGCAACTGTGAAA 60  
DB 1304 GGAGAGAAATGTGACTGTGGCGCTCTCGCAATCCGTCCTGGATGCTGCAACTGTGAAA 1363  
QY 61 CTGAGACCAAGGGGCGCAGTGTGACAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 120  
DB 1364 CTGAGACCAAGGGGCGCAGTGTGACAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 1423  
QY 121 GAAGAGCAATATGCGCGAGTGGCAAGGGGTGATGATGATTACTGCAATGGCATA 180  
DB 1424 GAAGAGCAATATGCGCGAGTGGCAAGGGGTGATGATGATTACTGCAATGGCATA 1483  
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCGC 213  
DB 1484 TCTGCTGGCTGTCCAGAAATCCCTTCATGCGC 1516

RESULT 7  
AY551929 270 bp mRNA linear VRT 24-JUN-2004  
LOCUS  
DEFINITION  
AY551929  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Gloydius blomhoffi breviaudus  
Gloydius blomhoffi breviaudus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Gloydius.  
1 (bases 1 to 270)  
Wang, J.H., Wu, Y., Ren, F. and Zhao, B.C.  
Cloning and characterization of adinitor: a novel disintegrin from  
a snake venom  
Unpublished  
2 (bases 1 to 270)  
Zhao, B.C., Wang, J.H., Ren, F. and Wu, Y.  
Direct Submission  
Submitted (19-FEB-2004) Department of Biochemistry and Molecular  
Biology, Dalian Medical University, 465 Zhongshan Road, Dalian,  
Liaoning 116027, China  
location/Qualifiers  
1..270  
/organism="Gloydius blomhoffi breviaudus"  
/mol\_type="mRNA"  
/sub\_species="brevicaudus"  
/db\_xref="taxon:259325"  
/cissue\_type="venom gland"  
1..270  
/function="inhibits platelet aggregation and angiogenesis"  
/note="contains a disintegrin-like domain"  
/codon\_start=1  
/product="adinitor"

CDS

ORIGIN

Query Match 93.2%; Score 198.6; DB 5; Length 270;  
Best Local Similarity 95.8%; Pred. No. 1.8e-52;  
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGTGACTGTGGCGCTCTCGCAATCCGTCCTGGATGCTGCAACTGTGAAA 60  
DB 16 GGAGAGAAATGTGACTGTGGCGCTCTCGCAATCCGTCCTGGATGCTGCAACTGTGAAA 75  
QY 61 CTGAGACCAAGGGGCGCAGTGTGACAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 120  
DB 76 CTGAGACCAAGGGGCGCAGTGTGACAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 135  
QY 121 GAAGAGCAATATGCGCGAGTGGCAAGGGGTGATGATGATTACTGCAATGGCATA 180  
DB 136 GAAGAGCAATATGCGCGAGTGGCAAGGGGTGATGATGATTACTGCAATGGCATA 195  
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCGC 213  
DB 196 TCTGCTGGCTGTCCAGAAATCCCTTCATGCGC 228

RESULT 8  
AF054626 318 bp mRNA linear VRT 01-APR-1998  
LOCUS  
DEFINITION  
AF054626  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Gloydius blomhoffi breviaudus  
Gloydius blomhoffi breviaudus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Gloydius.  
1 (bases 1 to 318)  
Kang, I.C., Chung, K.H., Lee, S.J., Yun, Y.D., Moon, H.M. and Kim, D.S.  
Purification and molecular cloning of a platelet aggregation  
inhibitor from the snake (Agkistrodon halys breviaudus) venom  
Thromb. Res. (1998) In press  
2 (bases 1 to 318)  
Kang, I.C., Chung, K.H., Lee, S.J., Yun, Y.D., Moon, H.M. and Kim, D.S.  
Direct Submission  
Submitted (19-MAR-1998) Biochemistry, Yonsei University, College of  
Science, 134 Seodaemong-Gu, Shinchon-dong, Seoul 120-749, Korea  
location/Qualifiers  
1..318  
/organism="Gloydius blomhoffi breviaudus"  
/mol\_type="mRNA"  
/sub\_species="brevicaudus"  
/db\_xref="taxon:259325"  
1..318  
/gene="salmosin"  
1..318  
/gene="salmosin"  
/product="platelet aggregation inhibitor disintegrin"  
/protein\_id="AAC08997.1"  
/db\_xref="GI:3003025"  
/translation="MFTIMKQKPCILINKPLRTDTPVSPVSGNELLEAGEECDCSPG  
NRCDDATKLRGAGACAGLCCDCGRFKKEKTRRRARGDDLDCYKNGISAGCRNP  
FHA"

CDS

ORIGIN

Query Match 93.2%; Score 198.6; DB 5; Length 318;  
Best Local Similarity 95.8%; Pred. No. 1.8e-52;  
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY	1	GGAGAGAAGATGGA	CTGTGGGCGCTCTCTCAATCCGTGTGGATGCTGCAACCTGTAA	60
Db	103	GGAGAAGAAATG	GA	162
QY	61	CTGAACCAAGGCGCG	AGTGTGTCAGAAAGACTGTGTGTGACCAAGTGCAGATTATGAA	120
Db	163	CTGAACAAGAGGCA	CAGGTGTGCAGAAAGACTGTGTGTGACCAAGTGCAGATTATGAA	222
QY	121	GAAGAACAAATATG	CGCGGTGTCAGAGGGGTATGACATGATGATTAATGCAATGGCATA	180
Db	223	GAGGAACAATATG	CGCGGTGTCAGAGGGGTATGACATGATGATTAATGCAATGGCATA	282
QY	181	TCTGCTGGCTGTCC	CGAAGATCCCTTCATGCC	213
Db	283	TCTGCTGGCTGTCC	CGAAGATCCCTTCATGCC	315
RESULT 9				
LOCUS	AF367868			
DEFINITION	AF367868	972 bp	mRNA	linear
ACCESSION	AF367868			
VERSION	AF367868.1	GI:14794942		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
SOURCE				
gene				
CDS				
ORIGIN				
Query Match	93.2%	Score 198.6	DB 5	Length 972
Best Local Similarity	95.8%	Pred. No. 1.8e-52		
Matches	204	Conservative	0	Mismatches 9
				Indels 0
				Gaps 0
QY	1	GGAGAGAAGATGGA	CTGTGGGCGCTCTCTCAATCCGTGTGGATGCTGCAACCTGTAA	60
Db	739	GGAGAAGATGATGTG	CGCTCTCTCTGAAATCCGTGTGTGATGCTGCAGAACTGTAA	798
QY	61	CTGAACCAAGGCGCG	AGTGTGTCAGAAAGACTGTGTGTGACCAAGTGCAGATTATGAA	120
Db	799	CTGAGACAAGAGGCA	CAGTGTGTCAGAAAGACTGTGTGTGACCAAGTGCAGATTATGAA	858
QY	121	GAAGAACAAATATG	CGCGGTGTCAGAGGGGTATGACATGATGATTAATGCAATGGCATA	180

Db		869	GAGGAAACAATATGCCGGAGAGCAAGGGCGTATTAACCTGGAATGATTACTGAAATGCAGATA	918
Qy		181	TCTGCTGGCTGTCCCAAGAATCCTTCATGCC	213
Db		919	TCTGCTGGCTGTCCCAAGAATCCTTCATGCC	951
RESULT	10			
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Glomydus halys (halys viper)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Lepidodontaia; Squamata; Sclerozoosia; Serpentes; Colubridae;				
Viperidae; Crotalinae; Glomydus.				
1 (bases 1 to 1558)				
Fujisawa, Y., Kuroda, S., Notoya, K., Konishi, H. and Terashita, Z.				
Halystatin, a novel disintegrin from agkistrodon halys, is a potent				
inhibitor of bone resorption and platelet aggregation				
J. Takeda Res. Lab. 53, 39-56 (1994)				
2 (bases 1 to 1558)				
Kuroda, S.				
Direct Submission				
Submitted (08-MAR-1994) Shun-ichi Kuroda, Osaka University,				
Institute of Scientific and Industrial Research, Department of				
Structural Molecular Biology, 8-1 Mihogaoka, Ibaraki, Osaka				
567-0047, Japan (E-mail: skuroda@sanken.osaka-u.ac.jp,				
Tel:81-6-6879-8462, Fax:81-6-6879-8464)				
Location/Qualifiers				
FEATURES				
source				
1..1558				
/organism="Glomydus halys"				
/mol_type="mRNA"				
/db_xref="taxon:8714"				
/clone="lambda 16-33"				
/tissue_type="venom gland"				
/clone_id="lambda gtl1"				
10..1152				
/codon_start=1				
/product="prepro-halystatin"				
/protein_id="BAA06025.1"				
/db_xref="GI:469190"				
/translation="MIQVLITICLAVFPQGSIIVDSGNLEFEVVEYKVTALPR				
AAYNKEDAMQYFKNVGEPLILHLERNGLFSDYSLSHPDAEISAYSVEDH				
CFHYRVENDADSPASLSCDGKAHKIKIGEMWLLPELVSDPDAAVKREVENKE				
DEPRMGCVTONMSVESSTKKSGIANTVPOGSRPPGFITLAIYVHGWTAKGNEE				
RIRKHOMINNIIMCRALNITYSLSELIWSKDLITNASAPSELTPGANRETIV				
LINTSHDHQLMTALI FNSGVNLGRAVVGCDPKRSVAIVRHNALFTVAVMTEH				
MGNHGMHEDEKCNCTCMISKVLSOPSEFSDCENENYQTVVDHSQCILNDPL				
RPIDVSTPVSGNELLEGESDCDGS PENPCDDAATCKLRQAQACAEGLCCDOGRFMKK				
GYVRIRARGDDMDYDCNGISAGCPBNPFHA"				
10..63				
577..1182				
/product="hemorrhagin region"				
1183..1149				
/product="disintegrin region"				
ORIGIN				
Query Match				
Blast Local Similarity	95.8%	Pred	No. 1.7e-52;	
Matches	204;	Conservative	0;	Mismatches 9;
				Indels 0;
				Gaps 0;
Qy		1	GGAGAGAATGTGACTGTGGCGCTCCTGCAAAATCCGTGCTGCAGTAGCTGCAACCTGTAAA	60
Db		1237	GGAGAGAATGTGACTGTGGCGCTCCTGCAAAATCCGTGCTGCAGTAGCTGCAACCTGTAAA	1296
Qy		61	CTGAGACCAGGGGGCGAGTGTCGCAAGAGCATGTGTTGTGACCAAGTGCAGATTATTAATAA	120
Db		1297	CTGAGACCAGGGGGCGAGTGTCGCAAGAGCATGTGTTGTGACCAAGTGCAGATTATTAATAA	1356

QY 121 GAAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 180  
DB 1357 AAGAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 1416  
QY 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
DB 1417 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 1449

RESULT 11  
E05552 1558 bp RNA linear PAT 29-SEP-1997  
LOCUS E05552  
DEFINITION cDNA encoding platelet aggregation inhibiting polypeptide, halystatin.  
ACCESSION E05552  
VERSION E05552.1 GI:2173740  
KEYWORDS JP 1993255395-A/1.  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 1558)  
AUTHORS Fujisawa, Y. and Kuroda, S.  
TITLE POLYPEPTIDE AND ITS PRODUCTION  
JOURNAL Patent: JP 1993255395-A 1 05-OCT-1993;  
COMMENT TAKEDA CHEM IND LTD  
OS Agkistrodon halys blomhoffi (AHB)  
PN JP 1993255395-A/1  
PD 05-OCT-1993  
PF 03-OCT-1991 JP 1991256234  
PR 26-OCT-1990 JP 90P 287116, 20-FEB-1991 JP 91P 26328 PI  
FUJISAWA YUKIO, KURODA SHUNICHI  
PC C07K15/04, C07K13/00, C12N15/12, C12P21/02//A61K37/02, A61K37/02;

FEATURES  
source 1..1558  
Location/Qualifiers  
1..1558  
/organism="unclassified"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:32644"  
ORIGIN  
Query Match 93.2%; Score 198.6; DB 6; Length 1558;  
Best Local Similarity 95.8%; Pred. No. 1.7e-52;  
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GGAAGAGATGTGATCTGTGGCGCTCTCTGCAATTCGCTGCGATGCTGCACCTGTAA 60  
DB 1237 GGAAGAGATGTGATCTGTGGCGCTCTCTGCAATTCGCTGCGATGCTGCACCTGTAA 1236  
QY 61 CTGAGACGAGGGGCGAGTGTGCAGAGGACTGTGTGACCACTGAGATTTATGAAA 120  
DB 1297 CTGAGACGAGGGGCGAGTGTGCAGAGGACTGTGTGACCACTGAGATTTATGAAA 1356  
QY 121 GAAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 180  
DB 1357 AAGAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 1416  
QY 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
DB 1417 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 1449

RESULT 12  
AX009242 222 bp DNA linear PAT 06-SEP-2000  
LOCUS AX009242  
DEFINITION Sequence 3 from Patent EP0967276.

ACCESSION AX009242  
VERSION AX009242.1 GI:9996575  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Kang, I.C., Kim, D.S. and Chung, K.H.  
TITLE Anti-tumor agent comprising salmosin  
JOURNAL Patent: EP 0967276-A 3 29-DEC-1999;  
KIM DOO SIK (KR)  
FEATURES  
source 1..222  
Location/Qualifiers  
1..222  
/organism="Gloydius blomhoffi breviaudus"  
/mol\_type="unassigned DNA"  
/sub\_species="brevicaudus"  
/db\_xref="taxon:259325"  
ORIGIN  
Query Match 92.5%; Score 197; DB 6; Length 222;  
Best Local Similarity 95.3%; Pred. No. 5.8e-52;  
Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 1 GGAAGAGATGTGATCTGTGGCGCTCTCTGCAATTCGCTGCGATGCTGCACCTGTAA 60  
DB 7 GGAAGAGATGTGATCTGTGGCGCTCTCTGCAATTCGCTGATGCTGCACCTGTAA 66  
QY 61 CTGAGACGAGGGGCGAGTGTGCAGAGGACTGTGTGACCACTGAGATTTATGAAA 120  
DB 67 CTGAGACGAGGGGCGAGTGTGCAGAGGACTGTGTGACCACTGAGATTTATGAAA 126  
QY 121 GAAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 180  
DB 127 GAAGAACATATGCCGAGTGCAGAGGGGTGATGATCATGATGATTAATCATGAGCATTA 186  
QY 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213  
DB 187 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 219

RESULT 13  
AF367867 917 bp mRNA linear VRT 17-JUL-2001  
LOCUS AF367867  
DEFINITION Gloydius halys breviaudus metalloproteinase-like (hxl) mRNA.  
ACCESSION AF367867  
VERSION AF367867.1 GI:14794940  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Kallian, H.  
TITLE Direct Submission  
JOURNAL Submitted (02-APR-2001) Biochemistry, Guangxi Medical University, 6 Shuangyong Road, Nanning, Guangxi 530021, China  
COMMENT NBI staff are still waiting for submitters to provide appropriate coding region information.  
FEATURES  
source 1..917  
Location/Qualifiers  
1..917  
/organism="Gloydius blomhoffi breviaudus"  
/mol\_type="mRNA"  
/sub\_species="brevicaudus"  
/db\_xref="taxon:259325"  
<1..917  
/gene="hxl"  
/note="similar to metalloproteinase"  
ORIGIN

Query Match 92.5%; Score 197; DB 5; Length 917;  
 Best Local Similarity 95.3%; Pred. No. 5.7e-52;  
 Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 60  
 DB 702 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 761  
 QY 61 CTGAGACCAAGGAGGCGCACTGTGCAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 120  
 DB 762 CTGAGACCAAGGAGGCGCACTGTGCAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 821  
 QY 121 GAAGGAAACAATATGCCGATGCGAGAGGGGTATGACATGATGATTAATGCAATGGCATA 180  
 DB 822 GAAGGAAACAATATGCCGATGCGAGAGGGGTATGACATGATGATTAATGCAATGGCATA 881  
 QY 181 TCTGCTGGCTGTCCCGAAGAAATCCCTTCATGCC 213  
 DB 882 TCTGCTGGCTGTCCCGAAGAAATCCCTTCATGCC 914

RESULT 14  
 AF051788 2027 bp mRNA linear VRT 05-JAN-1999  
 LOCUS AF051788  
 DEFINITION Gloydius halys metalloprotease (Mt-b) mRNA, complete cds.  
 ACCESSION AF051788  
 VERSION AF051788.1 GI:4106002  
 KEYWORDS  
 SOURCE Gloydius halys (halys viper)  
 ORGANISM Gloydius halys  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 Viperidae; Crotalinae; Gloydius.  
 1 (bases 1 to 2027)  
 JOURNAL Ueda, O.H. and Kim, D.S.  
 Direct Submission  
 Submitted (03-MAR-1998) Biochemistry, Yonsei University, 134  
 Shinchon-Dong Seodaemun-Gu, Seoul 120-749, Korea  
 FEATURES  
 source 1..2027  
 /organism="Gloydius halys"  
 /mol\_type="mRNA"  
 /strain="Brevicaudus"  
 /db\_xref="taxon:8714"  
 /tissue\_type="venom"  
 1..2027  
 /gene="Mt-b"  
 19..1536  
 /gene="Mt-b"  
 /codon\_start=1  
 /product="metalloprotease"  
 /protein\_id="AAD02653.1"  
 /db\_xref="GI:4106003"  
 /translation="MIQVILVITICLAVPPYQSSIIILSGNVVDYEVYPRKVTALPK  
 GAVQPYEDAMQYERKVGAEAVVHLERKKGLFSBDYSETHYSPGRBITTPYVEDH  
 CYHGRIONDASTASISACNGLKGFRLQGETYLIEPLKLSNEAAVTKYEDVEKE  
 DEAPRWCGVTONWESYEPIKEDVEKEDAEAKMGVQWNESEYPIKKAQSUNLTPAH  
 QRYELIVADHGMFKYNGSDKIRBWRQMTVADEIYSYMTIDVALGLQIWSNK  
 DLINVOAPAHTLDSFGKWRBRLHLRHHNNALMLAIDFGDTIGLAVGTMSNK  
 GSTGVQDHSITINRVATMAHEIGHNGLIHHDGSSCGSGYSIMSPVISHMSKXK  
 SDGSYTCQMDIINOKPQCLIKPLRTDVTSPVSGNELLAEAGECDGSGRPNPCDA  
 ATCKLRQAQCAELCCDQCQCFMEGTICRRGRDDIDYICNGISACCPNPPHA"

ORIGIN  
 Query Match 92.5%; Score 197; DB 5; Length 2027;  
 Best Local Similarity 95.3%; Pred. No. 5.7e-52;  
 Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 60  
 DB 1321 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 1380  
 QY 61 CTGAGACCAAGGCGCACTGTGCAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 120

Db 1381 CTGAGACCAAGGAGGCGCACTGTGCAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 1440  
 QY 121 GAAGGAAACAATATGCCGATGCGAGAGGGGTATGACATGATGATTAATGCAATGGCATA 180  
 DB 1441 GAAGGAAACAATATGCCGATGCGAGAGGGGTATGACATGATGATTAATGCAATGGCATA 1500  
 QY 181 TCTGCTGGCTGTCCCGAAGAAATCCCTTCATGCC 213  
 DB 1501 TCTGCTGGCTGTCCCGAAGAAATCCCTTCATGCC 1533

RESULT 15  
 AB059572 1983 bp mRNA linear VRT 10-OCT-2001  
 LOCUS AB059572  
 DEFINITION Trimeresurus elegans mRNA for elegantin-2a precursor, complete cds.  
 ACCESSION AB059572  
 VERSION AB059572.1 GI:15991221  
 KEYWORDS  
 SOURCE Trimeresurus elegans  
 ORGANISM Trimeresurus elegans  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 Viperidae; Crotalinae; Trimeresurus.  
 1  
 Shimozaka, S.  
 Trimeresurus elegans mRNA for elegantin-2a precursor, complete cds  
 JOURNAL Published Only in Database (2001)  
 2 (bases 1 to 1983)  
 Muraizama, N. and Shimozaka, S.  
 Direct Submission  
 Submitted (09-APR-2001) Nobuhito Muraizama, Showa University, School  
 of Pharmaceutical Sciences, 1-5-8 Hatanodai, Shingawa-ku, Tokyo  
 142-8555, Japan (e-mail: muraizama@pharm.showa-u.ac.jp,  
 Tel:81-3-3784-8203, Fax:81-3-3784-7550)  
 FEATURES  
 source 1..1983  
 /organism="Trimeresurus elegans"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:88086"  
 /sex="female"  
 /tissue\_type="venom gland"  
 73..1518  
 /codon\_start=1  
 /product="elegantin-2a precursor"  
 /protein\_id="BAB69658.1"  
 /db\_xref="GI:15991222"  
 /translation="MIQVILVITICLAVPPYQSSIIILSGNVVDYEVYPRKVTALPK  
 GAVQPYEDAMQYERKVGAEAVVHLERKKGLFSBDYSETHYSPGRBITTPYVEDH  
 CYHGRIONDASTASISACNGLKGFRLQGETYLIEPLKLSNEAAVTKYEDVEKE  
 DEAPRWCGVTONWESYEPIKEDVEKEDAEAKMGVQWNESEYPIKKAQSUNLTPAH  
 QRYELIVADHGMFKYNGSDKIRBWRQMTVADEIYSYMTIDVALGLQIWSNK  
 DLINVOAPAHTLDSFGKWRBRLHLRHHNNALMLAIDFGDTIGLAVGTMSNK  
 GSTGVQDHSITINRVATMAHEIGHNGLIHHDGSSCGSGYSIMSPVISHMSKXK  
 SDGSYTCQMDIINOKPQCLIKPLRTDVTSPVSGNELLAEAGECDGSGRPNPCDA  
 ATCKLRQAQCAELCCDQCQCFMEGTICRRGRDDIDYICNGISACCPNPPHA"  
 mat\_peptide 1297..1515  
 /product="disintegrin elegantin-2a"  
 640..1248  
 /note="metalloprotease-like domain"  
 1962..1967  
 polyA\_signal 1983  
 /note="19 A nucleotides"

ORIGIN  
 Query Match 91.7%; Score 195.4; DB 5; Length 1983;  
 Best Local Similarity 94.8%; Pred. No. 1.8e-51;  
 Matches 202; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 60  
 DB 1303 GGAGAGAAATGATGAGTGGCGCTCCGCAATCCGCTCCGATGCTGCAACTGTGAAA 1362







```
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCB1_Taxid=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashta Z.;
RT "Halysaticin, a novel disintegrin from agkistrodon halys, is a potent
RT inhibitor of bone resorption and platelet aggregation.";
RL Takeda Kenyusho Ho 53:39-56 (1994).
DR EMBL: D28871; BAA06027.1; -.
DR MEROPS: M12.134; -.
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Peptidase_M12B.
DR Pfam: PF00200; Disintegrin_1.
DR Pfam: PF01421; Reprolysin; 1.
DR PRINTS: PR00289; Disintegrin.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS50215; ADAM_MERPO; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
FT NON_TER
SQ SEQUENCE 117 AA; 12686 MW; B1F9A98056B807B CRC64;

Query Match
Best Local Similarity 99.3%; Score 430; DB 2; Length 117;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 60
DB 45 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 104
QY 61 GISACCPNPFHA 73
DB 105 GISACCPNPFHA 117

RESULT 3
Q9PVK9 PRELIMINARY; PRT; 482 AA.
AC Q9PVK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Metalloprotease.
GN Name=Mc-d;
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCB1_Taxid=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=brevicaudus; TISSUE=Venom;
RX MEDLINE=993337693; PubMed=10406963;
RA Jeon O.H., Kim D.S.;
RT "Molecular cloning and functional characterization of a snake venom
RT metalloprotease.";
RL Eur. J. Biochem. 263:526-533 (1999).
DR EMBL: AF051789; AAD02654.1; -.
DR HSP: P18619; 1FVL.
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Peptidase_M12B.
DR InterPro: IPR002870; Peptidase_M12B_N.
DR InterPro: IPR006025; Pept M_Zn_BS.
DR Pfam: PF00200; Disintegrin_1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
```

```
DR Pfam: PF01421; Reprolysin; 1.
DR PRINTS: PR00289; Disintegrin.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS50215; ADAM_MERPO; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Metalloprotease; Protease.
SQ SEQUENCE 482 AA; 53409 MW; C6014BBE87BC8B15 CRC64;

Query Match
Best Local Similarity 98.4%; Score 426; DB 2; Length 482;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 60
DB 410 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 469
QY 61 GISACCPNPFHA 73
DB 470 GISACCPNPFHA 482

RESULT 4
Q80124 PRELIMINARY; PRT; 77 AA.
AC Q80124;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Disintegrin (fragment).
OS Bothrops alternatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCB1_Taxid=64174;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramos O.H.P., Selistre-de-Araujo H.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY259516; AA075107.1; -.
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR00200; Disintegrin; 1.
DR PRINTS: PR00289; Disintegrin.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
KM Integrin.
FT NON_TER
SQ SEQUENCE 77 AA; 8179 MW; 680501C26E7ED496 CRC64;

Query Match
Best Local Similarity 97.0%; Score 420; DB 2; Length 77;
Matches 69; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 60
DB 5 EAGEBCDCCGAPNPPCCDAATCTLRPGACAGELCCDCCRFMKEGTICMARGDMDYCN 64
QY 61 GISACCPNPFHA 73
DB 65 GISACCPNPFHA 77

RESULT 5
Q7S2D5 PRELIMINARY; PRT; 73 AA.
AC Q7S2D5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
```

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DS Disintegrin (Fragment).  
OS Agkistrodon calliginosus (Korean viper) (Gloydius ussuriensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_Taxid=35671;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Snake venom gland;  
RA Sun D.-U., Yang T.-S.,  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY204249; AAP20644.1;  
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.  
DR InterPro; IPR01762; Disintegrin.  
DR Pfam; PF00200; Disintegrin; 1.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00500; DISIN; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
KW Integrin.  
FT NON TER 1  
SQ SEQUENCE 73 AA; 7768 MW; 615509DF966882EF CRC64;  
  
Query Match 94.7%; Score 410; DB 2; Length 73;  
Best Local Similarity 91.8%; Pred. No. 7,2e-34;  
Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEECDCDSPPNCCDATTCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60  
Dy 61 GISAGCPRNPFHA 73  
Db 61 GISAGCPRNPFHA 73  
  
RESULT 6  
Q7SZD9 PRELIMINARY; PRT; 478 AA.  
ID Q7SZD9;  
AC Q7SZD9;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DS Metalloprotease/disintegrin ussuri.  
OS Agkistrodon calliginosus (Korean viper) (Gloydius ussuriensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_Taxid=35671;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Snake venom gland;  
RA Sun D.-U., Yang T.-S.,  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY204245; AAP20640.1;  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR Pfam; PF00200; Disintegrin; 1.  
DR Pfam; PF01562; Pept\_M12B\_propep; 1.  
DR Pfam; PF01421; Peptolysin; 1.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00500; DISIN; 1.  
DR PROSITE; PS50215; ADAM\_MEPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Integrin.

SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;  
  
Query Match 94.7%; Score 410; DB 2; Length 478;  
Best Local Similarity 91.8%; Pred. No. 3.7e-33;  
Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60  
DB 406 EAGEECDCDSPPNCCDATTCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 465  
Dy 61 GISAGCPRNPFHA 73  
Db 466 GISAGCPRNPFHA 478  
  
RESULT 7  
Q78CP2 PRELIMINARY; PRT; 105 AA.  
ID Q78CP2;  
AC Q78CP2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DS Platelet aggregation inhibitor disintegrin (Fragment).  
OS Agkistrodon halys brevicaudus (Korean siamasa snake) (Gloydius halys brevicaudus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_Taxid=259325;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kang I.C., Chung K.H., Lee S.U., Yun Y.D., Moon H.M., Kim D.S.,  
RT Purification and molecular cloning of a platelet aggregation  
RT inhibitor from the snake (Agkistrodon halys brevicaudus) venom.  
RL Thromb. Res. 0:0-0(1998).  
DR EMBL; AF054626; AAC08997.1;  
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR000519; P\_crefoil.  
DR Pfam; PF00200; Disintegrin; 1.  
DR PRINTS; PR00680; PTFEFOIL.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00500; DISIN; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
KW Integrin.  
FT NON TER 1  
SQ SEQUENCE 105 AA; 11407 MW; 6F10AD4496DD35F2 CRC64;  
  
Query Match 94.5%; Score 409; DB 2; Length 105;  
Best Local Similarity 93.2%; Pred. No. 1.2e-33;  
Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60  
DB 33 EAGEECDCDSPPNCCDATTCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 92  
Dy 61 GISAGCPRNPFHA 73  
Db 93 GISAGCPRNPFHA 105  
  
RESULT 8  
Q90WC0 PRELIMINARY; PRT; 317 AA.  
ID Q90WC0;  
AC Q90WC0;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DS Metalloprotease (Fragment).  
GN Name=hxl-1;

```

OS Agkistrodon halys brevicaudus (Korean stamose snake) (Gloydus halys
OS brevicaudus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydus.
OK NCBI_TaxID=259325;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=venom gland;
RA Xilian H.;
RU Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF367868; AAK73517.1; -.
DR PIR; A59409; A59409.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 317 AA; 35109 MW; 9851177BCBE2202E CRC64;

Query Match 94.5%; Score 409; DB 2; Length 317;
Best Local Similarity 93.2%; Pred. No. 3.2e-33;
Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCKLRPGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 60
DB 245 EAGEECDCGSPNCPCCDATCKLRGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 304
QY 61 GISACPRNPFA 73
DB 305 GISACPRNPFA 317

RESULT 9
Q98SP2 PRELIMINARY; PRT; 477 AA.
ID 098SP2;
AC 098SP2;
DT 01-UN-2001 (TRENBLrel. 17, Created)
DT 01-UN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Bothriostatin.
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OK NCBI_TaxID=8724;
RN [1]
RP SEQUENCE FROM N.A.
RC Silva C.A., Martins de Camargo A.C., de Toledo Serrano S.M.;
RU Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF345931; AAK15542.1; -.
DR HSSP; P18619; IFVL.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT SIGNAL 1
KW SIGNAL.
FT CHAIN 190 391 Potential.
FT CHAIN 392 480 Potential.
SQ SEQUENCE 480 AA; 53619 MW; 5CF5E6476511B3D7 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 480;
Best Local Similarity 91.8%; Pred. No. 4.6e-33;
Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCKLRPGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 60

```

```

DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 477 AA; 53440 MW; AC973EE767E10B3 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 477;
Best Local Similarity 93.1%; Pred. No. 4.6e-33;
Matches 67; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGEBCDCGAPANPCCDATCKLRPGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 61
DB 406 AGEBCDCGSPNCPCCDATCKLRPGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 465
QY 62 ISACPRNPFA 73
DB 466 ISACPRNPFA 477

RESULT 10
Q90220 PRELIMINARY; PRT; 480 AA.
ID Q90220;
AC Q90220;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Prepro-halystatin precursor.
OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydus halys
OS pallasi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydus.
OK NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Fujisawa Y., Kuroda S., Norioya K., Konishi H., Terashta Z.;
RT "Halystatin, a novel disintegrin from agkistrodon halys, is a potent
RT inhibitor of bone resorption and platelet aggregation.";
RL Takeda Kenkyusho Ho 53:39-56 (1994).
DR EMBL; D28870; BAA06025.1; -.
DR PIR; A59410; A59410.
DR PIR; A59411; A59411.
DR HSSP; P18619; IFVL.
DR MEROPS; M12_134; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT SIGNAL 1
KW SIGNAL.
FT CHAIN 190 391 Potential.
FT CHAIN 392 480 Potential.
SQ SEQUENCE 480 AA; 53619 MW; 5CF5E6476511B3D7 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 480;
Best Local Similarity 91.8%; Pred. No. 4.6e-33;
Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCKLRPGAQCAEGLCCDQCFMKEGTICMARGDMDYCN 60

```

```
Db 408 EAGEBCDGGSPNCCDAATCKLRGAQCAEGLCCDCCRFMKGTVCRIARGDDMDYCN 467
QY 61 GISAGCPNPFHA 73
Db 468 GISAGCPNPFHA 480

RESULT 11
ID 073795 PRELIMINARY; PRT; 505 AA.
AC 073795.
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Metalloprotease.
GN Name=Mt-B;
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydius.
OC NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=brevicaudus; TISSUE=Venom;
RA Ueon O.H., Kim D.S.;
RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051788; L. AAD02653.1; -.
DR HSSP; P18619; 1FVL.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin_1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin_1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRODOM; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Metalloprotease; Protease.
SQ SEQUENCE 505 AA; 5636 MW; C96B99FC9C05378F CRC64;

Query Match 93.5%; Score 405; DB 2; Length 505;
Best Local Similarity 91.8%; Pred. No. 1.2e-32;
Matches 67; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNCCDAATCKLRFGAQCAGLCCDCCRFMKGTTCRMARGDDMDYCN 60
Db 433 EAGEBCDGGSPNCCDAATCKLRGAQCAEGLCCDCCRFMKGTICRRGGDDLDYCN 492
QY 61 GISAGCPNPFHA 73
Db 493 GISAGCPNPFHA 505

RESULT 12
DISI_AGRHA STANDARD; PRT; 71 AA.
AC P21858;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin halysin (platelet aggregation activation inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
```

```
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91362676; PubMed=1889330;
RA Huang T.-F., Lin C.-S., Ouyang C.H., Teng C.-M.;
RT "Halysin, an antiplatelet Arg-Gly-Asp-containing snake venom peptide,
as fibrinogen receptor antagonist."
RL Biochem. Pharmacol. 42:1209-1219(1991).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
glycoprotein IIb-IIIa receptor on the platelet surface and
inhibits aggregation induced by ADP, thrombin, platelet-activating
factor and collagen.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
DR HSSP; P18619; 1FVL.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRODOM; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KM Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
FT DISULFID 47 66 By similarity.
FT SITE 51 53 Cell attachment site.
SQ SEQUENCE 71 AA; 7517 MW; E2B134B927155592 CRC64;

Query Match 91.7%; Score 397; DB 1; Length 71;
Best Local Similarity 91.5%; Pred. No. 1.4e-32;
Matches 65; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNCCDAATCKLRFGAQCAGLCCDCCRFMKGTTCRMARGDDMDYCN 60
Db 1 EAGEBCDGGSPNCCDAATCKLRGAQCAEGLCCDCCRFMKGTVCRIARGDDMDYCN 60
QY 61 GISAGCPNPF 71
Db 61 GISAGCPNPF 71

RESULT 13
DISI_AGRPI STANDARD; PRT; 71 AA.
AC P16318;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin aplaphin (platelet aggregation activation inhibitor).
OS Agkistrodon piscivorus piscivorus (Eastern cottonmouth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8716;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90046735; PubMed=2510158;
RA Chao B.H., Jakubowski U.A., Savage B., Ping Chow E., Marzec U.M.,
RA Harker U.A., Maraganore J.M.;
RT "Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a
potent inhibitor of platelet activation."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8050-8054(1989).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
glycoprotein IIb-IIIa receptor on the platelet surface and
inhibits aggregation induced by ADP, thrombin, platelet-activating
factor and collagen.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
```

CC -1- SIMILARITY: Belongs to the disintegrin family.  
DR PIR, A33990, A3390.  
DR HSP, P18619, 1FVU.  
DR InterPro, IPR001762; Disintegrin.  
DR Pfam, PF00200; Disintegrin, 1.  
DR PRINTS, PR00289; DISINTEGRIN.  
DR ProDom, PD000664; Disintegrin, 1.  
DR SMART, SM00050; DISIN, 1.  
DR PROSITE, PS00427; DISINTEGRIN\_1, 1.  
DR PROSITE, PS50214; DISINTEGRIN\_2, 1.  
DR Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.  
KM DISULFID 47 65 By similarity.  
FT SITE 50 52 Cell attachment site.  
SQ SEQUENCE 71 AA; 7522 MW; B514FDE47D67E266 CRC64;  
  
Query Match 90.6%; Score 392.5; DB 1; Length 71;  
Best Local Similarity 90.3%; Pred. No. 4e-32;  
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 EAGEBDCGAPNPPCDATCKLRGACACAGLCCDCCRFMKKEGTICRMARGDDMDPYCN 60  
DB 1 EAGEBDCGSPNPPCDATCKLRGACAGLCCDCCRFMKKEGTICRARGDDMDPYCN 59  
QY 61 GISACCPNPPH 72  
DB 60 GISACCPNPPH 71  
  
RESULT 14  
DISG\_TRIAB STANDARD; PRT; 73 AA.  
ID DISG\_TRIAB STANDARD; PRT; 73 AA.  
AC P62384; P17496; (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DE Disintegrin albolabrin (Platelet aggregation activation inhibitor).  
OC Trimeresurus albolabris (White-lipped pit viper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_Taxid=8765;  
RN [1]  
RP TISSUE=Venom;  
RC MEDLINE=90283463; PubMed=2191722;  
RA Williams J., Kucinski B., Holt J., Niewiarowski S.;  
RA "Elegantin and albolabrin purified peptides from viper venoms:  
RT homologues with the RGDs domain of fibrinogen and von Willebrand  
RL factor";  
RN Biochim. Biophys. Acta 1039:81-89(1990).  
RP DISULFIDE BONDS.  
RC TISSUE=Venom;  
RC MEDLINE=91242430; PubMed=2036389;  
RA Calvete J.J., Schaefer W., Soeska T., Lu W., Cook J.J., Jameson B.A.,  
RA Niewiarowski S.;  
RT "Identification of the disulfide bond pattern in albolabrin, an RGD-  
RT containing peptide from the venom of Trimeresurus albolabris:  
RT significance for the expression of platelet aggregation inhibitory  
RT activity";  
RN Biochemistry 30:5225-5229(1991).  
RN [3]  
RN STRUCTURE BY NMR.  
RP MEDLINE=94109384; PubMed=8281937;  
RA Jaseja M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,  
RA Hyde E.I.;  
RT "1H-NMR studies and secondary structure of the RGD-containing snake  
RT toxin, albolabrin";  
RN Eur. J. Biochem. 218:853-860(1993).  
RN [4]  
RN STRUCTURE BY NMR.  
RP MEDLINE=97052455; PubMed=8897089;  
RX Smith K.J., Jaseja M., Lu X., Williams J.A., Hyde E.I., Trayer I.P.;

RT "three-dimensional structure of the RGD-containing snake toxin  
RT albolabrin in solution, based on 1H NMR spectroscopy and simulated  
RT annealing calculations";  
RL Int. J. Pept. Protein Res. 48:220-228(1996).  
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors  
CC expressed on glycoprotein IIb-IIIa complex. Acts by binding to the  
CC glycoprotein IIb-IIIa receptor on the platelet surface and  
CC inhibits aggregation induced by ADP, thrombin, platelet-activating  
CC factor and collagen.  
CC SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -1- SIMILARITY: Belongs to the disintegrin family.  
DR PIR, A23731, A23731.  
DR HSP, P18619, 1FVU.  
DR InterPro, IPR001762; Disintegrin.  
DR Pfam, PF00200; Disintegrin, 1.  
DR PRINTS, PR00289; DISINTEGRIN.  
DR ProDom, PD000664; Disintegrin, 1.  
DR SMART, SM00050; DISIN, 1.  
DR PROSITE, PS00427; DISINTEGRIN\_1, 1.  
DR PROSITE, PS50214; DISINTEGRIN\_2, 1.  
DR Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.  
KM DISULFID 6 15 Probable.  
FT DISULFID 8 16 Probable.  
FT DISULFID 21 35 Probable.  
FT DISULFID 29 59 Probable.  
FT DISULFID 34 38 Probable.  
FT DISULFID 47 66  
FT SITE 51 53 Cell attachment site.  
SQ SEQUENCE 73 AA; 7573 MW; F7E011E2F46FEF14 CRC64;  
  
Query Match 90.3%; Score 391; DB 1; Length 73;  
Best Local Similarity 87.7%; Pred. No. 5.8e-32;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 EAGEBDCGAPNPPCDATCKLRGACACAGLCCDCCRFMKKEGTICRMARGDDMDPYCN 60  
DB 1 EAGEBDCGSPNPPCDATCKLRGACAGLCCDCCRFMKKEGTICRARGDDMDPYCN 60  
QY 61 GISACCPNPPH 73  
DB 61 GISACCPNPPH 73  
  
RESULT 15  
DISG\_TRIAB STANDARD; PRT; 73 AA.  
ID DISG\_TRIAB STANDARD; PRT; 73 AA.  
AC P62383; P17496; (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DE Disintegrin trigramin gamma (Platelet aggregation activation  
DE inhibitor).  
OC Trimeresurus gramineus (Indian green tree viper) (Green habu snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_Taxid=8767;  
RN [1]  
RP TISSUE=Venom;  
RC MEDLINE=90207217; PubMed=2320569;  
RA Dennis M.S., Henzel W.J., Pitti R.M., Lipari M.T., Napier M.A.,  
RA Deisher T.A., Bunting S., Lazarus R.A.;  
RT "Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms:  
RT evidence for a family of platelet aggregation inhibitors";  
RN Proc. Natl. Acad. Sci. U.S.A. 87:2471-2475(1990).  
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors  
CC expressed on glycoprotein IIb-IIIa complex. Acts by binding to the  
CC glycoprotein IIb-IIIa receptor on the platelet surface and  
CC inhibits aggregation induced by ADP, thrombin, platelet-activating  
CC factor and collagen.  
CC SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- SIMILARITY: Belongs to the disintegrin family.  
 DR PIR: E35982; E35982.  
 DR HSSP: P18619; 1FVL.  
 DR InterPro: IPR001762; Disintegrin.  
 DR Pfam: PF00200; Disintegrin\_1.  
 DR PRINTS: PRO0289; DISINTEGRIN.  
 DR PRODOM: PD000664; Disintegrin; 1.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS00427; DISINTEGRIN 1; 1.  
 DR PROSITE: PS0214; DISINTEGRIN 2; 1.  
 KW Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.  
 FT DISULFID 6 15 By similarity.  
 FT DISULFID 8 16 By similarity.  
 FT DISULFID 21 35 By similarity.  
 FT DISULFID 29 59 By similarity.  
 FT DISULFID 34 38 By similarity.  
 FT DISULFID 47 66 By similarity.  
 FT SITE 51 53 Cell attachment site.  
 SQ SEQUENCE 73 AA; 7573 MW; F7B01E2F46FEF14 CRC64;

Query Match 90.3%; Score 391; DB 1; Length 73;  
 Best Local Similarity 87.7%; Pred. No. 5.8e-32;  
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGACAGELCCDCCRFMKETICRMARGDDMDYCN 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 EAGEDCCDGGSPANPCDAATCKLLPGACGGELCCDCCSFMKGTICRRARGDDLDYCN 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GISAGCPRRNPFA 73  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 GISAGCPRRNPFA 73  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: December 3, 2004, 21:38:11  
 Job time : 137 secs

**This Page Blank (uspio)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 3, 2004, 20:08:42 ; Search time 116 Seconds

(without alignments)  
225.752 Million cell updates/sec

Title: US-10-089-473A-1

Perfect score: 453  
Sequence: 1 EAGEECDGAPANPCDDAAT.....DMDDYNGISAGCPNPFHA 73

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 segs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: Genesecp23Sep04:\*  
2: genesecp1980s:\*  
3: genesecp2000s:\*  
4: genesecp2001s:\*  
5: genesecp2002s:\*  
6: genesecp2003as:\*  
7: genesecp2003bs:\*  
8: genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	433	100.0	73	5	AAE19787
2	409	94.5	73	5	AAW14083
3	409	94.5	73	5	AAV58231
4	409	94.5	73	5	AAE19791
5	409	94.5	480	2	AAK42867
6	402	92.8	73	5	AAK06494
7	392.5	90.6	71	5	AAU75225
8	391	90.3	73	2	AAK06395
9	391	90.3	73	2	AAK10106
10	391	90.3	73	2	AAK53946
11	391	90.3	73	2	AAW45500
12	391	90.3	73	2	ADH67966
13	391	90.3	73	3	ABK20598
14	391	90.3	73	5	ABG30392
15	391	90.3	73	7	ABU63163
16	390	90.3	73	8	ADM10975
17	390	90.1	96	2	AAK28703
18	390	90.1	96	2	AAK28707
19	390	90.1	97	2	AAK28704
20	390	90.1	97	2	AAK28706
21	390	90.1	99	2	AAK25153
22	390	90.1	99	2	AAK25149
23	390	90.1	106	2	AAK25148
24	390	90.1	106	2	AAK25152
25	387	89.4	97	2	AAK28705

26	387	89.4	97	2	AAK28708
27	387	89.4	98	2	AAK25154
28	387	89.4	98	2	AAK25150
29	386.5	89.3	71	2	AAK53942
30	384	88.7	96	2	AAK25151
31	384	88.7	96	2	AAK25382
32	384	88.7	96	2	AAK25147
33	382	88.2	72	1	AAK25120
34	379	87.5	73	2	AAK10110
35	379	87.5	73	2	ADK65996
36	375	86.6	72	2	AAK10109
37	372.5	86.0	71	2	ADK66000
38	371.5	85.8	73	2	AAK53937
39	371	85.7	72	2	ADK65998
40	368	85.0	483	3	AAV79413
41	368	85.0	483	4	AAE03036
42	360	83.1	478	5	ABG70857
43	356	82.2	72	2	AAK46215
44	356	82.2	72	2	AAK46218
45	356	82.2	72	2	AAW50453

## ALIGNMENTS

RESULT 1	AAE19787	
ID	AAE19787 standard; protein; 73 AA.	
XX		
AC	AAE19787;	
XX		
DT	29-AUG-2003 (revised)	
DT	07-AUG-2003 (revised)	
DT	18-JUN-2002 (first entry)	
XX		
DE	Agkistrodon saxatilis emelianov saxatillin protein.	
XX		
KW	Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;	
KW	platelet aggregation; angiogenesis; cytotoxicity.	
OS	Glycydinus halys.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1..3	
FT		note="Encoded by GGA"
XX		
FN	WO200214488-A1.	
XX		
PD	21-FEB-2002.	
XX		
PF	26-JUL-2000; 2000WO-KR000809.	
XX		
PR	26-JUL-2000; 2000WO-KR000809.	
XX		
PA	(CHUN/) CHUNG K.	
PA	(KIMD/) KIM D.	
PI	Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;	
DR	WPI, 2002-241803/29.	
DR	N-PSDB; AAD31060.	
XX		
PT	New CDNA encoding Saxatillin protein derived from venom of Korean snake	
PT	Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation	
PT	agent and anti-tumor agent.	
XX		
PS	Claim 2; Page 35; 41pp; English.	
XX		
CC	The invention relates to a CDNA encoding Saxatillin protein derived from	
CC	venom of Korean snake Agkistrodon saxatilis emelianov. The CDNA is useful	
CC	for as an anti-tumour agent and for effectively suppressing platelet	
CC	aggregation which makes it possible as and an active ingredient of anti-	
CC	platelet agent. Saxatillin is useful for inhibiting angiogenesis induced	

CC by tumour and for inhibiting tumour without cytotoxicity. The present  
 CC sequence is Agkistrodon saxatilis emeljanov saxatilis protein. (Updated  
 CC on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to  
 CC standardise OS field)

XX Sequence 73 AA;

Query Match 100.0%; Score 433; DB 5; Length 73;  
 Best Local Similarity 100.0%; Pred. No. 9, 2e-32;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60  
 DB 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60  
 QY 61 GISACGPRNPFHA 73  
 DB 61 GISACGPRNPFHA 73

RESULT 2  
 AAM14083  
 ID AAM14083 standard; peptide; 73 AA.

AC AAM14083;  
 DT 17-OCT-2003 (revised)  
 DT 27-OCT-1997 (first entry)

DE Platelet aggregation inhibitor, Salmosin.

KM Salmosin; inhibitor; blood; platelet aggregation; venom; Korean;  
 KM salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.

XX Gloydius halys brevicaudus.

XX FR2736266-A1.

XX 10-JAN-1997.

XX 24-AUG-1995; 95FR-00010049.

XX 05-JUL-1995; 95KR-00019685.

XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

PI In CK, Kwang HC, Soo JL, Doo SK, Hak DK, Yung DY, Jeong HY;  
 PI Hong KM;

XX WPI; 1997-121376/12.

PT Peptide derived from Korean salmosa viper venom - useful as blood  
 PT platelet aggregation inhibitor, for the management of thrombosis.

XX Claim 1; Page 11; 15pp; French.

CC This peptide, designated Salmosin, inhibits blood platelet aggregation.  
 CC It is derived from the venom of the Korean salmosa viper (Agkistrodon  
 CC halys brevicaudus). Salmosin can be used, in particular, in compositions  
 CC for management of thrombosis. Salmosin also has higher activity than  
 CC kistrin, gamma-triglycamin and echistatin. (Updated on 17-OCT-2003 to  
 CC standardise OS field)

XX Sequence 73 AA;

Query Match 94.5%; Score 409; DB 2; Length 73;  
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;  
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60  
 DB 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISACGPRNPFHA 73  
 DB 61 GISACGPRNPFHA 73

RESULT 3  
 AAY58231  
 ID AAY58231 standard; protein; 73 AA.

XX AAY58231;

DT 12-SEP-2003 (revised)  
 DT 27-MAR-2000 (first entry)

DE Korean snake venom salmosin.

KM Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;  
 KM metastasis; cancer; tumour.

XX Gloydius halys.

FT Key Location/Qualifiers  
 FT Region 51..53  
 FT /note="RGD motif"

XX EP667276-A2.

XX 29-DEC-1999.

XX 23-JUN-1999; 99EP-00304935.

XX 23-JUN-1998; 98KR-00023378.  
 XX 04-JUN-1999; 99KR-00020579.

XX (KIMD/) KIM D.

XX Kim D, Chung KH, Kang I;

XX WPI: 2000-064611/06.

XX N-PSDB; AAZ55609.

XX Novel polypeptides used for antitumor therapy.  
 XX Claim 1; Page 13; 24pp; English.

CC This sequence represents a 7.5 kD salmosin protein of a Korean snake,  
 CC Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of  
 CC small proteins mainly derived from snake venom which contain an RGD or  
 CC RGD motif (the structural motif recognised by platelet fibrinogen  
 CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of  
 CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,  
 CC the former being a marker of angiogenic blood vessels and certain  
 CC malignant cells. Disintegrins inhibit tumour metastasis by blocking  
 CC tumour cell adhesion to the extracellular matrix, and antagonism of  
 CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.  
 CC Salmosin can be used as an anticancer agent. It may be used for the  
 CC inhibition or reduction of tumour cell angiogenesis, the inhibition of  
 CC metastatic tumour formation and the inhibition or reduction of metastatic  
 CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy  
 CC applications. Many types of cancer may be treated with salmosin or  
 CC nucleotides encoding it, including leukaemia and cancers of the breast,  
 CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain,  
 CC muscle and bone. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 73 AA;

Query Match 94.5%; Score 409; DB 3; Length 73;  
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;  
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60  
 DB 1 EAGEBCDGGAPNPPCCDAATCKLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISAGCPNPFHA 73  
 DB 61 GISAGCPNPFHA 73

RESULT 4  
 AAE19791  
 ID AAE19791 standard; protein, 73 AA.

XX AAE19791;  
 AC 29-AUG-2003 (revised)  
 DT 18-JUN-2002 (first entry)  
 XX

DE Agkistrodon halys brevicaudus salmosin protein.  
 XX Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;  
 KM platelet aggregation; angiogenesis; salmosin; cytotoxicity.

XX Gloydius halys brevicaudus.

XX WO20021448-A1.

XX 21-FEB-2002.

XX 26-JUL-2000; 2000WO-KR000809.

XX 26-JUL-2000; 2000WO-KR000809.

XX (CHUN/) CHUNG K.

XX (KIMD/) KIM D.

XX Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;

XX WPI; 2002-241903/29.

PT New cDNA encoding Saxatillin protein derived from venom of Korean snake  
 PT Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation  
 PT agent and anti-tumor agent.

XX Example 5; Page 38-39; 41pp; English.

XX The invention relates to a cDNA encoding Saxatillin protein derived from  
 CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful  
 CC for as an anti-tumour agent and for effectively suppressing platelet  
 CC aggregation which makes it possible as and an active ingredient of anti-  
 CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced  
 CC by tumour and for inhibiting tumour without cytotoxicity. The present  
 CC sequence is Agkistrodon halys brevicaudus salmosin protein. (Updated on  
 CC 29-AUG-2003 to standardise OS field)

XX Sequence 73 AA;

Query Match 94.5%; Score 409; DB 5; Length 73;  
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;  
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNCCDAATCKLRPGAQCAEGLCCDCCRFMKGTTCRMARGDDMDYCN 60  
 DB 1 EAGEBCDCCGSPGNPCDAATCKLRPGAQCAEGLCCDCCRFMKGTTCRRARGDDLDYCN 60

QY 61 GISAGCPNPFHA 73  
 DB 61 GISAGCPNPFHA 73

RESULT 5  
 AAR42867  
 ID AAR42867 standard; protein, 480 AA.

XX AAR42867;  
 XX

DT 24-OCT-2003 (revised)  
 DT 11-MAY-1994 (first entry)

XX Platelet aggregation inhibitory peptide.

XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.

XX Gloydius halys blomhoffi.

XX JP05255395-A.

XX 05-OCT-1993.

XX 03-OCT-1991; 91UP-00256234.

XX 26-OCT-1990; 90UP-00287116.

XX 20-FEB-1991; 91UP-00026328.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1993-348481/44.

XX N-PSDB; AAG50394.

XX Polypeptide of specified aminoacid sequence - used for inhibiting  
 PT platelet aggregation caused by e.g. collagen, thrombin, etc.

XX Example; Page 33-35; 50pp; Japanese.

CC The sequence is that of a polypeptide which inhibits platelet aggregation  
 CC caused by ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on  
 CC 24-OCT-2003 to standardise OS field)

XX Sequence 480 AA;

Query Match 94.5%; Score 409; DB 2; Length 480;  
 Best Local Similarity 91.8%; Pred. No. 6.5e-29;  
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNCCDAATCKLRPGAQCAEGLCCDCCRFMKGTTCRMARGDDMDYCN 60  
 DB 408 EAGEBCDCCGSPGNPCDAATCKLRPGAQCAEGLCCDCCRFMKGTTCRRARGDDLDYCN 467

QY 61 GISAGCPNPFHA 73  
 DB 468 GISAGCPNPFHA 480

RESULT 6  
 AAR06494  
 ID AAR06494 standard; protein, 73 AA.

XX AAR06494;

XX 25-MAR-2003 (revised)

DT 04-JAN-1991 (first entry)

XX Platelet aggregation inhibitor.

XX Snake venom; thromboxan A2; thrombosis; anti-coagulant.

XX Synthetic.

XX WO9008772-A.

XX 09-AUG-1990.

XX 27-JAN-1989; 89US-00303585.

XX 27-JAN-1989; 89US-00303585.

XX 01-NOV-1989; 89US-00430313.

XX (UYBO-) UNIV BOSTON.

PA (BIOJ) BIOGEN INC.  
 XX  
 PI Maraganore J, Jakubowski J, Chao B;  
 XX WPL 1990-260891/34.  
 DR N-PSDB; AA005730.  
 XX  
 PT Pure platelet activation inhibiting polypeptide from snake venom - used  
 PT for preventing agglutination and release in vivo or vitro, and new  
 PT recombinant dna encoding it.  
 XX  
 PS Claim 3; Fig 9; 73pp; English.  
 XX  
 CC The sequence is deduced from the coding strand of a synthetic gene for a  
 CC polypeptide inhibitor of platelet activation. The polypeptide is  
 CC analogous to that obtd. from the venom of Agkistrodon p. piscivorus  
 CC (North American Water Moccasin). The gene can be used to produce  
 CC recombinant inhibitor or fusion proteins with eg. hirudin derivs. These  
 CC can be used to decrease/ inhibit platelet aggregation and release in vivo  
 CC or in vitro. Usual dose is 0.01-100 mg/kg body wt. The recombinant  
 CC protein can also be used to coat the surfaces of invasive medical  
 CC devices. It can also block stenosis and spasm at the site of thrombosis (  
 CC by inhibiting the release of thromboxan A2 ). See also AAR06508. (Updated  
 CC on 25-MAR-2003 to correct PA field.)  
 CC  
 SO Sequence 73 AA;  
 Query Match 92.8%; Score 402; DB 2; Length 73;  
 Best Local Similarity 90.3%; Pred. No. 5.7e-29;  
 Matches 65; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EAGEECDCGAPNPPCCDAATCTLRPGACCAEGCCDCCRFMKKEGTCRMAGDDMDVDCN 60  
 DB 2 EAGEECDCGSPNPPCCDAATCTLRPGACCAEGCCDCCRFMKKEGTCRRARGDDVNDYCN 61  
 QY 61 GISACGPRNPFH 72  
 DB 62 GISACGPRNPFH 73  
 RESULT 7  
 AAU75225  
 ID AAU75225 standard; protein; 71 AA.  
 XX  
 AC AAU75225;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE Agkistrodon piscivorus protein #2 relating to albumin fusion proteins.  
 XX  
 KW Albumin fusion protein; therapeutic protein; immune disorder;  
 KW autoimmune disorder; blood-related disorder; hyperproliferative disorder;  
 KW renal disorder; cardiovascular disorder; respiratory disorder;  
 KW neurological disorder; endocrine disorder; reproductive system disorder;  
 KW gastrointestinal disorder; infectious disease; wound healing;  
 KW human serum albumin; HSA; HA.  
 XX  
 OS Agkistrodon piscivorus.  
 XX  
 PN WO200179271-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US012009.  
 XX  
 PR 12-APR-2000; 2000US-0229358P.  
 PR 25-APR-2000; 2000US-0199384P.  
 PR 21-DEC-2000; 2000US-0256931P.  
 XX  
 PA (PRIN-) PRINCIPAL PHARM CORP.  
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
 XX  
 PI Balance DJ, Sleep D, Turner AJ, Sadeghi H, Prior CP;

XX  
 DR WPI; 2002-179329/23.  
 XX  
 PT New albumin fusion proteins with extended shelf life, useful for treating  
 PT leukemia, warts, hepatitis, multiple sclerosis and AIDS, comprises  
 PT therapeutic protein fused to albumin.  
 XX  
 PS Disclosure; Page 336; 338pp; English.  
 XX  
 CC The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein and albumin (e.g. human serum albumin (HSA or HA)).  
 CC The albumin fusion proteins are useful for treating, preventing, or  
 CC ameliorating various disorders. Such disorders include immune disorders,  
 CC autoimmune disorders, blood-related disorders, hyperproliferative  
 CC disorders, renal disorders, cardiovascular disorders, respiratory  
 CC disorders, neurological disorders, endocrine disorders, reproductive  
 CC system disorders, gastrointestinal disorders, infectious disease, and  
 CC wound healing. Therapeutic proteins can be stabilised to extend shelf  
 CC life and/or retain the protein's activity for extended periods of time in  
 CC solution, in vivo or in vitro by genetically or chemically fusing the  
 CC protein to albumin or its fragment or variant. In addition the use of  
 CC albumin fusion proteins reduces the need to formulate protein solutions  
 CC with large excesses of carrier proteins to prevent loss of therapeutic  
 CC protein due to factors such as binding to the container. The extension of  
 CC shelf life was tested by measuring biological activity (MD2 cell  
 CC proliferation) of human albumin-human growth hormone (HA-hGH) fusion  
 CC protein remaining after incubation in cell culture media for up to 3  
 CC weeks. At week 3 there was still approximately 95% cell proliferation  
 CC compared to no activity of unused hGH. The present sequence represents  
 CC an Agkistrodon piscivorus protein of unknown function. Note: The present  
 CC sequence is given in the sequence listing but is not mentioned elsewhere  
 CC in the specification  
 CC  
 SO Sequence 71 AA;  
 Query Match 90.6%; Score 392.5; DB 5; Length 71;  
 Best Local Similarity 90.3%; Pred. No. 4e-28;  
 Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 EAGEECDCGAPNPPCCDAATCTLRPGACCAEGCCDCCRFMKKEGTCRMAGDDMDVDCN 60  
 DB 1 EAGEECDCGSPNPPCCDAATCTLRPGACCAEGCCDCCRFMKKEGTCRRARGDDVNDYCN 59  
 QY 61 GISACGPRNPFH 72  
 DB 60 GISACGPRNPFH 71  
 RESULT 8  
 AAR06395  
 ID AAR06395 standard; protein; 73 AA.  
 XX  
 AC AAR06395;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-DEC-1990 (first entry)  
 XX  
 DE Albolabrin.  
 XX  
 KW Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;  
 KW Viper venom.  
 XX  
 OS Trimeresurus albolabris.  
 XX  
 PN EP382451-A.  
 XX  
 PD 16-AUG-1990.  
 XX  
 PR 05-FEB-1990; 90EP-00301181.  
 PR 07-FEB-1989; 89US-00307642.  
 XX  
 PA (MERI) MERCK & CO INC.

PA (UTEM) UNIV TEMPLE.  
 PA (FRIE) FRIEDMAN P A.  
 XX Friedmann PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;  
 PI Niewiarowski S, Holt JC, Rucinski B;  
 XX WPI, 1990-248351/33.  
 DR  
 XX Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to  
 PT human platelets and inhibiting fibrinogen-induced aggregation.  
 XX  
 PS Claim 2; Page 13; 13pp; English.  
 CC The peptide is prep. from the venom of the viper T. albolabris or may be  
 CC prep. by genetic engineering or solid phase synthesis. It inhibits both  
 CC fibrin binding to human platelets and fibrinogen-induced aggregation of  
 CC human platelets. It is eliminated from the circulation rapidly and is  
 CC therefore useful in situations where a strong antithrombotic action of  
 CC short duration is needed, e.g. in surgery on peripheral arteries, in  
 CC cardiovascular surgery and the interaction of platelets with artificial  
 CC surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 CC  
 XX Sequence 73 AA;  
 SQ  
 Query Match 90.3%; Score 391; DB 2; Length 73;  
 Best Local Similarity 87.7%; Pred. No. 5.6e-28;  
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60  
 DB 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60  
 QY 61 GISAGCPRNPFFHA 73  
 DB 61 GISAGCPRNPFFHA 73  
 RESULT 9  
 AAR10106  
 ID AAR10106 standard; protein; 73 AA.  
 AC AAR10106;  
 XX  
 DT 13-MAR-1991 (first entry)  
 XX  
 DE Trigaminin-gamma.  
 XX  
 KW Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition;  
 KW GP IIA; GP IIA; hypercoagulation.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9015072-A.  
 XX  
 PD 13-DEC-1990.  
 XX  
 PF 07-JUN-1989; 89US-00362718.  
 XX  
 PR 07-JUN-1989; 89US-00362718.  
 XX  
 PA (GETH) GENENTECH INC.  
 XX  
 PI Lazarus R, Dennis M;  
 XX  
 DR WPI, 1991-007159/01.  
 DR N-PSDB; AAR10160.  
 XX  
 PT Platelet aggregation inhibiting amino acid sequences - are derived from  
 PT snake venom and inhibit fibrinogen binding to GP IIA-GP IIA.  
 XX  
 PS Disclosure; Fig 1; 91pp; English.  
 XX

CC The sequence was produced by recombinant techniques using a synthetic  
 CC gene prep. from 10 oligonucleotides based on the amino acid sequence  
 CC determined by Edman degradation. The recombinant trigaminin-gamma is used  
 CC in treatment of hypercoagulation-related states. See also AAR10107-R10113  
 XX  
 SQ Sequence 73 AA;  
 Query Match 90.3%; Score 391; DB 2; Length 73;  
 Best Local Similarity 87.7%; Pred. No. 5.6e-28;  
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60  
 DB 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60  
 QY 61 GISAGCPRNPFFHA 73  
 DB 61 GISAGCPRNPFFHA 73  
 RESULT 10  
 AAR53946  
 ID AAR53946 standard; peptide; 73 AA.  
 AC AAR53946;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Distintegrin peptide #14.  
 XX  
 KW Distintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen;  
 KW integrin binding sites; GP IIB/IIIA; human; platelets; radiolabel;  
 KW treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;  
 KW tumours; abscesses; thrombus component.  
 XX  
 OS Trimeresurus albolabris.  
 XX  
 PN WO9409036-A1.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 05-OCT-1993; 93WO-US009523.  
 XX  
 PR 19-OCT-1992; 92US-00965674.  
 XX  
 PA (UTEM) UNIV TEMPLE.  
 XX  
 PI Knight LC, Maurer AH;  
 XX  
 DR WPI, 1994-151248/18.  
 XX  
 PT Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) - for  
 PT treatment and diagnosis of venous and arterial thrombi, pulmonary emboli  
 PT and tumours or abscesses having a thrombus component.  
 XX  
 PS Claim 28; Page 48; 62pp; English.  
 XX  
 CC The sequences given in AAR53933-46 are disintegrin peptides. Disintegrins  
 CC are low molecular weight proteins from the Viperidae family of snakes  
 CC which bind integrin proteins similar to the endogenous messenger and  
 CC structurally interactive molecules. Disintegrins are competitive  
 CC inhibitors of biomolecules, such as fibrinogen, for integrin binding  
 CC sites such as GP IIB/IIIA on human platelets. Disintegrins contain the  
 CC tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can  
 CC be used for the treatment and diagnosis of venous and arterial thrombi,  
 CC pulmonary emboli and tumours or abscesses that have a thrombus component.  
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX  
 SQ Sequence 73 AA;  
 XX

Query Match 90.3%; Score 391; DB 2; Length 73;  
Best Local Similarity 87.7%; Pred. No. 5,6e-28;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEEDCGAPNPPCCDAATCTLRPGACACAGLCCDQGRFMKEGTCGMARAGDDMDYCN 60  
DB 1 EAGEEDCGSPNPPCCDAATCTLRPGACGEGELCCDQCSFMKGTICRRARAGDDLDYCN 60

OY 61 GISACGPRNPFHA 73  
DB 61 GISACGPRNPLHA 73

RESULT 11  
AAW45500  
ID AAW45500 standard; peptide; 73 AA.  
XX AAW45500;  
AC  
XX  
XX 20-MAY-1998 (first entry)  
DT  
XX  
XX Albolabrin peptide targeting ligand.  
DE  
XX Contrast agent; targeted composition; diagnosis; diseased tissue;  
KM glycoprotein GPIIb/IIIa receptor; albolabrin.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9640285-A1.  
PN  
XX  
XX 19-DEC-1996.  
PD  
XX  
XX 06-JUN-1996; 96WO-US009938.  
PF  
XX  
XX 07-JUN-1995; 95US-00497684.  
PR 01-MAY-1996; 96US-00640464.  
XX  
XX  
XX (IMAR-) IMARX PHARM CORP.  
PA  
XX  
XX Unger EC, Shen D, Wu G;  
PI  
XX  
XX WPI; 1997-077233/07.  
DR  
XX  
XX Contrast agent or targeted compsn. for imaging or treating diseased  
PT tissue - comprising lipid, protein or polymer, a gas, and a targeting  
PT ligand e.g. a protein, peptide, saccharide or steroid.

XX  
XX Disclosure; Page 57; 175pp; English.  
PS  
XX  
XX This sequence represents a targeting ligand. The invention relates to a  
CC contrast agent for diagnostic imaging or a target composition which  
CC comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination  
CC with (iii) a targeting ligand (TL). TL targets cells or receptors  
CC selected from myocardial, endothelial, epithelial and tumour cells and  
CC the glycoprotein GPIIb/IIIa receptor. Also claimed are: a composition  
CC comprising vesicles containing (i) - (iii) and an aqueous carrier; a  
CC targeted vesicle composition comprising a fluorinated gas and a targeting  
CC ligand (TL) which targets tissues or receptors; a formulation for  
CC therapeutic or diagnostic use comprising (i)-(iii) and a bioactive agent;  
CC and a method for providing an image of an internal region of a patient,  
CC or for diagnosing the presence of diseased tissue, comprising: (a)  
CC administration of a composition as above; and (b) scanning the patient  
CC using ultrasound to obtain a visible image of the region of diseased  
CC tissue. The methods and compounds are useful for imaging or diagnosing  
CC the presence of diseased tissue, especially myocardial, endothelial or  
CC epithelial tissue but also gastrointestinal and cardiovascular regions.  
CC In particular the ligand targets regions of arteriosclerosis. Stabilised  
CC vesicles are particularly useful for perfusion imaging. The vesicles may  
CC also be used to deliver active agents to an intended target such as  
CC tissue or a receptor, and ultrasound can then be used to promote rupture  
CC of the vesicles and release a bioactive or diagnostic agent  
XX  
XX Sequence 73 AA;  
SQ

Query Match 90.3%; Score 391; DB 2; Length 73;  
Best Local Similarity 87.7%; Pred. No. 5,6e-28;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEEDCGAPNPPCCDAATCTLRPGACACAGLCCDQGRFMKEGTCGMARAGDDMDYCN 60  
DB 1 EAGEEDCGSPNPPCCDAATCTLRPGACGEGELCCDQCSFMKGTICRRARAGDDLDYCN 60

OY 61 GISACGPRNPFHA 73  
DB 61 GISACGPRNPLHA 73

RESULT 12  
ADH67966  
ID ADH67966 standard; peptide; 73 AA.  
XX ADH67966;  
AC  
XX  
XX 25-MAR-2004 (first entry)  
DT  
XX  
XX Composition targeting ligand peptide Albolabrin.  
DE  
XX  
XX bioactive agent; anionic lipid; cationic counter ion;  
KM lipid covalently bonded to a polymer; ultrasound; charged lipid;  
KM targeted drug delivery; diagnostic imaging; targeting ligand;  
KM GPIIb/IIIa receptor; diagnosis; vascular thrombosis; clot.  
XX  
XX Unidentified.  
OS  
XX  
XX WO9842383-A1.  
PN  
XX  
XX 01-OCT-1998.  
PD  
XX  
XX 25-FEB-1998; 98WO-US003632.  
PF  
XX  
XX 21-MAR-1997; 97US-00823791.  
PR 06-MAY-1997; 97US-00851780.  
PR 18-JUN-1997; 97US-00877826.  
PR 02-JUL-1997; 97US-00887215.  
PR 08-SEP-1997; 97US-00925353.  
XX  
XX (IMAR-) IMARX PHARM CORP.  
PA  
XX  
XX Unger EC,  
PI  
XX  
XX WPI; 1998-557028/47.  
DR  
XX  
XX Processes for drug delivery, therapeutic imaging and diagnostic imaging -  
PT comprises use of compositions comprising charged lipid, counterion and  
PT lipid covalently bonded to polymer.

XX  
XX Disclosure; Page 68; 167pp; English.  
PS  
XX  
XX The invention relates to a method of: (A) delivering a bioactive agent  
CC (BA) to a patient by: (a) administering a composition comprising: (i) an  
CC anionic lipid (AL); (ii) a cationic counter ion (CCI); (iii) a lipid  
CC covalently bonded to a polymer (LBP), and (iv) BA, and (b) applying  
CC therapeutic ultrasound to facilitate delivery of BA in a desired region;  
CC (B) delivering a BA to a patient, comprising administering a composition  
CC comprising a charged lipid (CL), a counter ion (CI), LBP, BA and  
CC targeting ligand (TL); (C) providing an image of an internal region of a  
CC patient, comprising: (a) administering a composition comprising CL, CI  
CC and LBP of the composition in (B), and (b) scanning the patient using  
CC diagnostic imaging, to give visible images of the region, and (D)  
CC contrast agent comprising components as in (Ca). The  
CC compositions/processes described above may be used in drug delivery.  
CC targeted drug delivery, therapeutic imaging and diagnostic imaging. This  
CC sequence represents an example of a targeting ligand designated  
CC Albolabrin.  
XX  
XX Sequence 73 AA;  
SQ



Db 1 EAGEBCDCCGAPANPCCDATCKLBPAGCGEGLCDDCCSFMKGTICRRAGDDDDYCN 60  
QY 61 GISAGCPNPFHA 73  
Db 61 GISAGCPNPLHA 73

## RESULT 15

ABU63163 standard; protein; 73 AA.

ABU63163;

17-SEP-2003 (first entry)

Targeting ligand #13 used in novel diagnostic ultrasound method.

ultrasound method; targeted vesicle composition; targeting ligand;  
ultrasound scanning; dual frequency ultrasound insonation; micelle;  
liposome; phospholipid; ultrasound energy; vesicle oscillation;  
reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus;  
endothelial tissue; epithelial cell; tumour cell; myocardial cell;  
integrin; malignancy; inflammation; heart; diseased tissue; imaging;  
gastrointestinal region; lymphatic system.

Synthetic.

US6521211-B1.

18-FEB-2003.

03-FEB-1999; 99US-00243640.

07-JUN-1995; 95US-00497684.

01-MAY-1996; 96US-00640464.

06-JUN-1996; 96US-00660032.

06-FEB-1998; 98US-0073913P.

22-DEC-1998; 98US-00218660.

(BRIM ) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.

Unger EC, Wu Y;

WPI, 2003-S31036/50.

Ultrasound diagnosis, by administering targeted vesicle composition with

vesicles encapsulating gas, in combination with targeting ligand, to a

patient, and scanning patient by dual frequency ultrasound insonation.

Disclosure; Col 50; 96pp; English.

The present invention relates to a novel ultrasound method which involves

administering to a patient a targeted vesicle composition which comprises

vesicles encapsulating a gas, in combination with a targeting ligand, and

scanning the patient using dual frequency ultrasound insonation. The

vesicles themselves comprise a lipid, protein or polymer, and are

selected from liposomes and micelles. The vesicles may comprise a

phospholipid selected from dioleoylphosphatidylcholine,

dimyristoylphosphatidylcholine, dipalmitoylphosphatidylcholine,

distearoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine,

dioleoylphosphatidylethanolamine, N-succinylidoleoylphosphatidylethanolamine, 1-hexadecyl-2-

palmitoyldioleoylphosphoethanolamine and phosphatidic acids. The method of

scanning involves exposing the patient to a first ultrasound energy,

and then subsequently, while the vesicle is oscillating, exposing the

patient to a second ultrasound energy having a second insonation

frequency that is different from the first insonation frequency, and

detecting the reflected ultrasound signal. The method is useful for

ultrasound diagnosis, for detection of a thrombus or enhancement of

thrombus (e.g. old or echogenic thrombus) and for detecting vesicles

targeted to epithelial cells, tumour cells, myocardial cells, and

endothelial tissue including integrins associated with malignancy or  
inflammation. The method is also useful for diagnosing the presence or  
absence of diseased tissue in a patient and for imaging one or more  
regions of a patient, such as for providing images of the heart,  
gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent  
targeting ligands that may be used in the method of the present invention

Sequence 73 AA;

Query Match

Best Local Similarity 87.7%; Score 391; DB 7; Length 73;

Best Local Similarity 87.7%; Pred. No. 5, 6e-28; Mismatches 5; Indels 0; Gaps 0;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPANPCCDATCKLBPAGCGEGLCDDCCSFMKGTICRRAGDDDDYCN 60

Db 1 EAGEBCDCCGAPANPCCDATCKLBPAGCGEGLCDDCCSFMKGTICRRAGDDDDYCN 60

QY 61 GISAGCPNPFHA 73

Db 61 GISAGCPNPLHA 73

Search completed: December 3, 2004, 21:35:44

Job time : 117 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:04:21 / Search time 408 Seconds  
(without alignments)  
2740.507 Million cell updates/sec

Title: US-10-089-473a-2  
Perfect score: 213  
Sequence: 1 ggaagaagaatgcgtgtg.....ccagaatccctccatgcc 213

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues  
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*  
1: Geneseq1988s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	213	6	AAD31060 Agkistrod
2	213	100.0	222	8	ACC44733 Agkistrod
3	198.6	93.2	1558	2	AAQ50394 Platelet
4	197	92.5	222	3	AAZ55609 Platelet
5	190.6	89.5	2029	5	AAZ94881 Southern
6	190.6	89.5	2029	5	AAZ94881 Southern
7	185.8	87.2	2102	6	ABSS4623 Disintegr
8	174.6	82.0	222	8	ACC47594 Disintegr
9	154.8	72.7	174	2	AAQ50357 pAgalphe2
10	153.2	71.9	174	2	AAQ44933 pAgalphe2
11	153.2	71.9	174	2	AAQ50385 Platelet
12	151.6	71.2	174	2	AAQ44932 pAgalphe1
13	151.6	71.2	174	2	AAQ50390 Platelet
14	151.6	71.2	174	2	AAQ50384 Platelet
15	150	70.4	174	2	AAQ44934 pAgalphe3
16	150	70.4	174	2	AAQ50386 Platelet
17	150	70.4	174	2	AAQ44939 pAgalphe8
18	150	70.4	174	2	AAQ44940 pAgalphe9
19	150	70.4	174	2	AAQ44938 pAgalphe7
20	150	70.4	174	2	AAQ50393 Platelet
21	150	70.4	174	2	AAQ44941 pAgalphe1

22	150	70.4	174	2	AAQ50391 Platelet
23	150	70.4	174	2	AAQ50392 Platelet
24	148.4	69.7	174	2	AAQ44936 pAgalphe5
25	148.4	69.7	174	2	AAQ50387 Platelet
26	148.4	69.7	174	2	AAQ44935 pAgalphe4
27	148.4	69.7	174	2	AAQ44937 pAgalphe6
28	148.4	69.7	174	2	AAQ50388 Platelet
29	148.4	69.7	174	2	AAQ50389 Platelet
30	144.6	67.9	598	6	ABK10642 Corticomou
31	143	67.1	908	6	ABK10648 Corticomou
32	135.4	63.6	1434	6	ABSS4624 Disintegr
33	125.8	59.1	226	2	AAQ05730 Platelet
34	124.2	58.3	1213	6	ABK10638 Pigmy rat
35	122.6	57.6	2334	6	ABK10644 Pigmy rat
36	122.4	57.5	229	2	AAQ10160 Trigramin
37	120	56.3	288	2	AAQ25315 Encodes b
38	119.6	56.2	288	2	AAQ25314 Encodes b
39	111.4	52.3	1851	5	AAQ85063 E. carina
40	111.4	52.3	1863	8	ABK93715 Human chr
41	111.4	52.3	1863	8	ABK93715 Human chr
42	106.4	50.0	333	6	ABK10649 Cotcomou
43	106.4	50.0	585	6	ABK10643 Cotcomou
44	101.2	47.5	2240	6	ABK14952 Korean ad
45	100.8	47.3	226	2	ADP66009 Snake ven

## ALIGNMENTS

RESULT 1  
AAD31060  
ID AAD31060 standard; cDNA, 213 bp.  
XX  
AC AAD31060;  
XX  
DT 29-AUG-2003 (revised)  
DT 07-AUG-2003 (revised)  
DT 18-JUN-2002 (first entry)  
XX  
DE Agkistrodon saxatilis emelianov saxatillin cDNA.  
XX  
XX Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;  
KM platelet aggregation; angiogenesis; cytotoxicity; ss.  
XX  
OS Glycydus halys.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..213  
FT /\*tag= a  
FT /product= "Saxatillin protein"  
FT /transl\_except= (pos:1..3, aa:Glu-Ala-Gly)  
FT /note= "Deletion of 6 bases alters the reading frame; CDS  
does not include start and stop codon"  
FT /partial  
XX  
XX WO200214488-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 26-JUL-2000; 2000WO-KR000809.  
XX  
XX 26-JUL-2000; 2000WO-KR000809.  
XX  
XX 26-JUL-2000; 2000WO-KR000809.  
XX  
XX (CHUN/) CHUNG K.  
XX (KIMD/) KIM D.  
XX  
XX Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;  
XX WPI; 2002-241903/29.  
XX P-FSDB; AAB19787.  
XX  
XX New cDNA encoding Saxatillin protein derived from venom of Korean snake  
PT Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation

PT agent and anti-tumor agent.  
XX  
PS Claim 1; Page 36; 41pp; English.  
XX  
CC The invention relates to a cDNA encoding Saxatillin protein derived from  
CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful  
CC for as an anti-tumor agent and for effectively suppressing platelet  
CC aggregation which makes it possible as an active ingredient of anti-  
CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced  
CC by tumor and for inhibiting tumor without cytotoxicity. The present  
CC sequence is Agkistrodon saxatilis emelianov saxatillin cDNA. (Updated on  
CC 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise  
CC OS field)  
XX  
SQ Sequence 213 BP; 56 A; 45 C; 65 G; 47 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 213; DB 6; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTGCTGCGATGCGAACCTGTAAA 60  
DB 1 GGAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTGCTGCGATGCGAACCTGTAAA 60  
XX  
QY 61 CTGAGACCAAGGGGCGGAGTGTGACAGAGACTGTGTGTGACCACTGAGATTATGAAA 120  
DB 61 CTGAGACCAAGGGGCGGAGTGTGACAGAGACTGTGTGTGACCACTGAGATTATGAAA 120  
XX  
QY 121 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 180  
DB 121 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 180  
XX  
QY 181 TCTGCTGGCTGTGCCAGAAATCCCTTCATGCC 213  
DB 181 TCTGCTGGCTGTGCCAGAAATCCCTTCATGCC 213  
XX  
RESULT 2  
ID ACC44733 standard; cDNA; 222 BP.  
XX  
AC ACC44733;  
XX  
DT 27-OCT-2003 (revised)  
DT 29-MAY-2003 (first entry)  
XX  
DE Agkistrodon saxatilis saxatillin cDNA sequence SEQ ID NO:1.  
XX  
KW Agkistrodon saxatilis; saxatillin; anti-cancer; cancer; disintegrin;  
KW tumor; lipoplex; cancer growth inhibition; cationic liposome;  
KW cytosolic; gene therapy; gene; ss.  
XX  
OS Glycydus halys.  
XX  
FN WO2003018065-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 29-AUG-2001; 2001WO-KR001461.  
XX  
PR 29-AUG-2001; 2001WO-KR001461.  
XX  
PA (CHUN/) CHUNG K.  
XX  
PI Chung K, Park Y, Kim S, Hong S, Sohn Y, Jang Y, Hun C, Kim D;  
XX  
DR MPI; 2003-278621/27.  
XX  
PT Lipoplex useful for inhibiting growth of cancer cells, and for treating  
PT or preventing cancer, comprises a cationic liposome and an expression  
PT vector containing the saxatillin gene.  
XX  
PS Claim 1; Page 20; 24pp; English.

XX  
CC The present invention describes a lipoplex for inhibiting cancer growth  
CC comprising a cationic liposome and an expression vector containing a  
CC saxatillin gene having a sequence of 222 base pairs (bp), given in  
CC ACC44733. Also described is a method for inhibiting cancer growth by  
CC using a saxatillin gene, which comprises: (a) mixing cholesterol with  
CC DOPAP, suspending the mixture in aqueous medium to prepare cationic  
CC liposome, and introducing saxatillin gene to eukaryotic vector; (b) mixing  
CC the cationic liposome and expression vector in aqueous medium and  
CC homogenising to prepare lipoplex; and (c) introducing the lipoplex to a  
CC cancer tissue. Saxatillin is a disintegrin gene which has cytostatic  
CC activity and can be used in gene therapy. The lipoplex is useful for  
CC inhibiting growth of cancer cells, and for treating or preventing cancer.  
CC (Updated on 27-Oct-2003 to standardise OS field)  
XX  
SQ Sequence 222 BP; 59 A; 47 C; 68 G; 48 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 213; DB 8; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTGCTGCGATGCGAACCTGTAAA 60  
DB 7 GGAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTGCTGCGATGCGAACCTGTAAA 66  
XX  
QY 61 CTGAGACCAAGGGGCGGAGTGTGACAGAGACTGTGTGTGACCACTGAGATTATGAAA 120  
DB 67 CTGAGACCAAGGGGCGGAGTGTGACAGAGACTGTGTGTGACCACTGAGATTATGAAA 126  
XX  
QY 121 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 180  
DB 127 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 186  
XX  
QY 181 TCTGCTGGCTGTGCCAGAAATCCCTTCATGCC 213  
DB 187 TCTGCTGGCTGTGCCAGAAATCCCTTCATGCC 219  
XX  
RESULT 3  
ID AA050394 standard; cDNA to mRNA; 1558 BP.  
XX  
AC AA050394;  
XX  
DT 24-OCT-2003 (revised)  
DT 11-MAY-1994 (first entry)  
XX  
DE Platelet aggregation inhibitory peptide.  
XX  
KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.  
XX  
OS Glycydus halys blomhoffi.  
XX  
FN Key Location/Qualifiers  
FT CDS 10..1452  
FT /tag= a  
XX  
PD JP05255395-A.  
XX  
PF 05-OCT-1993.  
XX  
PR 03-OCT-1991; 91JP-00256234.  
XX  
PR 26-OCT-1990; 90JP-00287116.  
XX  
PR 20-FEB-1991; 91JP-00026328.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
DR WPI; 1993-348481/44.  
XX  
DR P-FSDB; AAR42867.  
XX  
PT Polypeptide of specified aminoacid sequence - used for inhibiting  
PT platelet aggregation caused by e.g. collagen, thrombin, etc.

```
XX Example; Page 33-35; 50pp; Japanese.
XX
XX The sequence is that encoding a polypeptide which inhibits platelet
CC aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.
CC (Updated on 24-OCT-2003 to standardise OS field)
CC
XX Sequence 1558 BP; 468 A; 310 C; 362 G; 418 T; 0 U; 0 Other;
SO
Query Match          93.2%; Score 198.6; DB 2; Length 1558;
Best Local Similarity 95.8%; Pred. No. 3e-57;
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GGAGAGAATGTGACTGTGGCGCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 60
Db 1237 GGAGAAGAGTGTACTGTGCTCTCCGAAATCCGTGTGCGATGCTGCACCTGTAA 1296
QY 61 CTGAGACCGAGGCGCGAGTGTGCAGAGAGCTGTGTGACACAGTGCAGATTATGAAA 120
Db 1297 CTGAGACAGGCGGCGACAGTGTGCAGAGAGCTGTGTGACACAGTGCAGATTATGAAA 1356
QY 121 GAAGAAACAATATCCCGGATGGCAAGGGGTGATGATGATTACTGCATGGCAT 180
Db 1357 AAAAGAAACAATATCCCGGATGGCAAGGGGTGATGATGATTACTGCATGGCAT 1416
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 213
Db 1417 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 1449
RESULT 4
AAZ55609
ID AAZ55609 standard; cDNA; 222 BP.
XX
AC AAZ55609;
XX
DT 15-SEP-2003 (revised)
DT 27-MAR-2000 (first entry)
XX
DE Korean snake venom salmosin cDNA.
XX
KW Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;
KW metastasis; cancer; tumour; ss.
XX
OS Gloydius halys.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..219
FT /*tag= a
FT /product= "Korean snake salmosin"
XX
XX EP967276-A2.
XX
XX 29-DEC-1999.
XX
XX 23-JUN-1999; 99EP-00304935.
XX
XX 23-JUN-1998; 98KR-00023778.
XX 04-JUN-1999; 99KR-00020579.
XX
XX (KIMD/) KIM D.
XX
XX Kim D, Chung KH, Kang I;
XX
XX WPI, 2000-064611/06.
XX
XX P-P5DB; AAY58231.
XX
XX Novel polypeptides used for antitumor therapy.
XX
XX Claim 7; Page 14; 24pp; English.
XX
XX This sequence represents cDNA encoding the 7.5 kD salmosin protein of a
XX Korean snake, Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a
```

```
CC family of small proteins mainly derived from snake venom which contain an
CC RGD or KGD motif (the structural motif recognised by platelet fibrinogen
CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of
CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,
CC the former being a marker of angiogenic blood vessels and certain
CC malignant cells. Disintegrins inhibit tumour metastasis by blocking
CC tumour cell adhesion to the extracellular matrix, and antagonism of
CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.
CC Salmosin can be used as an anticancer agent. It may be used for the
CC inhibition or reduction of tumour cell angiogenesis, the inhibition of
CC metastatic tumour formation and the inhibition or reduction of metastatic
CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy
CC applications. Many types of cancer may be treated with salmosin or
CC nucleotides encoding it, including leukaemia and cancers of the breast,
CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain,
CC muscle and bone. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 222 BP; 62 A; 46 C; 66 G; 48 T; 0 U; 0 Other;
SQ
Query Match          92.5%; Score 197; DB 3; Length 222;
Best Local Similarity 95.3%; Pred. No. 4.7e-57;
Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGAGAGAATGTGACTGTGGCGCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 60
Db 7 GGAGAGAATGTGACTGTGGCGCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 66
QY 61 CTGAGACCGAGGCGCGAGTGTGCAGAGAGCTGTGTGACACAGTGCAGATTATGAAA 120
Db 67 CTGAGACAGAGGACACAGTGTGCAGAGAGCTGTGTGACACAGTGCAGATTATGAAA 126
QY 121 GAAGAAACAATATCCCGGATGGCAAGGGGTGATGATGATTACTGCATGGCAT 180
Db 127 GAAGAAACAATATCCCGGATGGCAAGGGGTGATGATGATTACTGCATGGCAT 186
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 213
Db 187 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 219
RESULT 5
AAZ94881
ID AAZ94881 standard; cDNA; 2029 BP.
XX
AC AAZ94881;
XX
DT 01-AUG-2000 (first entry)
DT
XX
DE Southern copperhead snake conortrostatin cDNA.
XX
XX
KW Southern copperhead snake; venom; conortrostatin; disintegrin;
KW cytostatic; antiproliferative; thrombolytic; cerebroprotective;
KW antiaggregant; antiarteriosclerotic; antitumoral; caridiac; metastasis;
KW thrombolysis; thromboembolism; stroke; arteriosclerosis; atherosclerosis;
KW embolism; aneurism; angina; myocardial infarction; integrin; ss.
XX
XX Agkistrodon conortrostix.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 87..1538
FT /*tag= a
FT /transl_except= (pos:1023..1025, aa:Ala)
FT polyA_signal 1988..1993
FT /*tag= b
FT polyA_site 2010..2020
FT /*tag= c
XX
XX WC0200018421-A1.
XX
XX 06-APR-2000.
XX
XX 29-SEP-1999; 99WC-US022608.
```

```

PR 29-SEP-1996; 98US-00163047.
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
XX Markland FS, Zhou Q;
XX
XX WPI, 2000-303389/26.
XX P-PSDB; AAY79413.
XX
XX Novel proteins and polynucleotides representing contorrostatin useful
XX for inhibiting platelet aggregation, tumor metastasis and growth.
XX
XX Claim 9; Fig 3A-D; 81pp; English.
XX
XX The present sequence is that of claimed DNA encoding the Southern
XX copperhead snake venom disintegrin, contorrostatin (see AAY79413), a
XX protein that inhibits the interactions between integrins and their
XX receptors. The DNA was obtained from a venom gland cDNA library by PCR
XX amplification using primers (see AAY79413-83) based on a conserved region
XX of disintegrins. Contorrostatin precursor protein includes a pro-protein
XX region, a metalloprotease region which includes a metal-binding motif,
XX and a disintegrin region which includes an RGD loop that acts as an
XX integrin antagonist. DNA molecules consisting of nucleotides 1341-1535
XX (encoding the disintegrin), 657-1316 (metalloprotease), 87-656 (pro-
XX protein) and 87-1535 (entire precursor protein) of the present sequence
XX are also claimed. These can be used in the recombinant production of
XX conorrostatin proteins. The purified proteins are used in
XX pharmaceutical compositions for treating diseases associated with an
XX integrin binding to an integrin receptor, especially to inhibit platelet
XX aggregation, tumor metastasis, angiogenesis, neovascularization, cell
XX adhesion, invasiveness, or growth (all claimed). The proteins are also
XX useful for treating a thrombotic disorder, e.g. preventing arterial,
XX venous, and microvascular thrombosis and thromboembolism, stroke,
XX transient ischaemic attacks, arteriosclerosis, atherosclerosis, pulmonary
XX embolism, aneurism, angina and myocardial infarction
XX
XX Sequence 2029 BP; 630 A; 433 C; 423 G; 543 T; 0 U; 0 Other;
SQ
Query Match 89.5%; Score 190.6; DB 3; Length 2029;
Best Local Similarity 93.4%; Pred. No. 1.8e-54;
Matches 199; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 GGAGAAAGATGTGACTGTGGCGCTCTCGCAATCCGTCGATGCTGCAACCTGTAAA 60
DB 1323 GGAGAAAGATGTGACTGTGGCGCTCTCGCAATCCGTCGATGCTGCAACCTGTAAA 1382
QY 61 CTGAGACCAAGGGCGCCAGTGTGCAAGAGACTGTGTGACCGATGCAATTTATGAAA 120
DB 1383 CTGACAAACAGGGTCAAGTGTGCAATGACTGTGTGACCGATGCAATTTATGAAA 1442
QY 121 GAAGAACAAATATGCCCGATGCAAGGGGTATGACATGATGATTAATGCAATGGCATA 180
DB 1443 GAAGAACAAATATGCCCGATGCAAGGGGTATGACATGATGATTAATGCAATGGCATA 1502
QY 181 TCTGTGGCTGTCCCAAAATCCCTTCATGCC 213
DB 1503 TCTGTGGCTGTCCCAAAATCCCTTCATGCC 1535

```

```

XX wound healing; ss.
XX
XX Agkistrodon conortrix.
XX
XX Key Location/Qualifiers
XX 5'UTR 1..86
XX /tag= a
XX misc_feature 87..656
XX /tag= b
XX /note= "Encodes proprotein of contorrostatin"
XX misc_feature 657..1316
XX /tag= c
XX /note= "Encodes metalloprotease of contorrostatin"
XX misc_feature 1341..1535
XX /tag= d
XX /note= "Encodes Disintegrin of contorrostatin"
XX 3'UTR 1539..2029
XX /tag= e
XX polyA_signal 1988..1993
XX /tag= f
XX
XX MO200141791-A1.
XX
XX 14-JUN-2001.
XX
XX 09-DEC-2000; 2000MCO-US033367.
XX
XX 10-DEC-1999; 99US-00460295.
XX 08-JUN-2000; 2000US-00591552.
XX
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
XX Markland FS, Zhou Q;
XX
XX WPI, 2001-381494/40.
XX P-PSDB; AAE03036.
XX
XX Homodimeric disintegrin useful for modulating the adhesion, motility, and
XX invasiveness of integrin expressing tumor cells.
XX
XX Example 5; Fig 3; 101pp; English.
XX
XX The present sequence is southern copper head snake cDNA encoding
XX contorrostatin (CN) protein. CN, a homodimeric disintegrin binds to
XX integrin alphabetas and induces alphabeta-mediated tyrosine
XX phosphorylation of CAS and FAK in tumour cells. CN is useful for
XX modulating the adhesion, motility, and invasiveness of integrin
XX expressing cells, preferably tumour cells and for inhibiting the adhesion
XX of integrin expressing cells to vitronectin. The pharmaceutical
XX composition comprising CN is useful for inhibiting platelet aggregation,
XX neovascularisation, angiogenesis, tumour metastasis, invasiveness or
XX growth, for inhibiting metastasis in melanoma, carcinoma and sarcoma
XX patients. It is also useful for treating thrombotic diseases,
XX osteoporosis, and wound healing in mammals
XX
XX Sequence 2029 BP; 630 A; 433 C; 423 G; 543 T; 0 U; 0 Other;
SQ
Query Match 89.5%; Score 190.6; DB 5; Length 2029;
Best Local Similarity 93.4%; Pred. No. 1.8e-54;
Matches 199; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 GGAGAAAGATGTGACTGTGGCGCTCTCGCAATCCGTCGATGCTGCAACCTGTAAA 60
DB 1323 GGAGAAAGATGTGACTGTGGCGCTCTCGCAATCCGTCGATGCTGCAACCTGTAAA 1382
QY 61 CTGAGACCAAGGGCGCCAGTGTGCAAGAGACTGTGTGACCGATGCAATTTATGAAA 120
DB 1383 CTGACAAACAGGGTCAAGTGTGCAATGACTGTGTGACCGATGCAATTTATGAAA 1442
QY 121 GAAGAACAAATATGCCCGATGCAAGGGGTATGACATGATGATTAATGCAATGGCATA 180
DB 1443 GAAGAACAAATATGCCCGATGCAAGGGGTATGACATGATGATTAATGCAATGGCATA 1502

```

QY 181 TCTGCTGCTGTCGCCAGAAATCCCTTCATGCC 213  
 DB 1503 TCTGCTGCTGTCGCCAGAAATCCCTTCATGCC 1535

RESULT 7  
 ABS54623  
 ID ABS54623 standard; cDNA; 2102 BP.  
 AC ABS54623;  
 XX  
 DT 28-NOV-2002 (first entry)  
 DE Disintegrin protease ZSNK16 cDNA.  
 XX  
 KW ss; gene; ZSNK16; disintegrin protease; antifertility; vulnery;  
 KW anticoagulant; thrombolytic; cell-matrix; cell-cell interaction;  
 KW cell proliferation; cell differentiation; immune recognition;  
 KW fertilisation; growth control; angiogenesis; fertility; tumour;  
 KW gamete maturation; immunology; coagulation; thrombosis; trauma;  
 KW epithelial disorder.  
 XX  
 OS Sistrurus miliarius.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 88..1524  
 FT /\*tag= a  
 FT /product= "ZSNK16"  
 FT sig\_peptide 88..141  
 FT /\*tag= b  
 FT misc\_feature 142..648  
 FT /\*tag= c  
 FT /note= "Encodes propeptide"  
 FT mat\_peptide 649..1521  
 FT /\*tag= d  
 FT /label= Mature\_ZSNK16  
 XX  
 PN MO200268458-A2.  
 XX  
 BD 06-SEP-2002.  
 XX  
 PF 20-FEB-2002; 2002MO-US004937.  
 XX  
 PR 20-FEB-2001; 2001US-0270276P.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 FI Fox B, Shepard PO;  
 XX  
 DR WPI; 2002-706967/76.  
 DR P-PSDB; ABG70857.  
 XX  
 PT New disintegrin protease (designated ZSNK16) homolog polypeptides, useful  
 PT in modulating cell-cell interactions, delivering therapeutic agents, or  
 PT as replacement therapy for e.g. fertility, coagulation, thrombosis or  
 PT trauma.  
 XX  
 PS Disclosure; Page 70-73; 77pp; English.  
 XX  
 CC The invention relates to a new isolated polypeptide, which is a  
 CC disintegrin protease designated ZSNK16 from Sistrurus miliarius,  
 CC comprising an integrin binding region (designated ZSNK16-1br) or a zinc-  
 CC binding motif (designated ZSNK16-zbm). Also included are the nucleic acid  
 CC encoding ZSNK16, a ZSNK16 expression vector a transformed cultured cell  
 CC expressing ZSNK16, producing anti-ZSNK16 antibodies, and a nucleic acid  
 CC encoding fusion proteins of the ZSNK16-1br and ZSNK16-zbm domains. The  
 CC polypeptide is useful as a tool for investigating cell-matrix and cell-  
 CC cell interactions, for studying cell proliferation or differentiation in  
 CC human tissues, for studying immune recognition, fertilisation, growth  
 CC control or angiogenesis, for identifying inhibitors of its activity, or  
 CC for delivering therapeutic agents (e.g. proteases, radionuclides,  
 CC chemotherapy agents or small molecules). The ZSNK16 polypeptide is also  
 CC useful as replacement therapy for disorders associated with cell-cell

CC interactions, e.g. fertility, gamete maturation, immunology, coagulation,  
 CC thrombosis, trauma or epithelial disorders. The polypeptide is also  
 CC useful in the development of antithrombotic and antineoplastic agents due  
 CC to their anti-adhesive, anti-migration of certain tumour cells, and anti-  
 CC angiogenesis activities. The antibodies to the ZSNK16 polypeptide are  
 CC useful for tagging cells that express ZSNK16, for isolating ZSNK16 by  
 CC affinity purification, for detecting or quantifying soluble ZSNK16 as  
 CC marker of underlying pathology or disease, or for screening expression  
 CC libraries. The present sequence encodes ZSNK16  
 XX  
 SQ Sequence 2102 BP; 656 A; 431 C; 442 G; 573 T; 0 U; 0 Other;  
 Query Match 87.2%; Score 185.8; DB 6; Length 2102;  
 Best Local Similarity 92.0%; Pred. No. 8,1e-53;  
 Matches 196; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGAGCTGTGGCGCTCCTGCAATCCGTGTGGAGATGCAACCTGTAA 60  
 DB 1309 GGAGAGAAATGAGCTGTGGCGCTCCTGCAATCCGTGTGGAGATGCAACCTGTAA 1368  
 QY 61 CTGAGACCAAGGCGCAGGTGTCAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 120  
 DB 1369 CTGAGACCAAGGCGCAGGTGTCAGAGAGACTGTGTGACCAAGTGCAGATTATGAAA 1428  
 QY 121 GAAGAACAAATATGCCGATGCGCAAGGGGTATGACATGAGATGATTCTGCATGGCATA 180  
 DB 1429 GAAGAACAAATATGCCGATGCGCAAGGGGTATGACATGAGATGATTCTGCATGGCATA 1488  
 QY 181 TCTGCTGCTGTCGCCAGAAATCCCTTCATGCC 213  
 DB 1489 TCTGCTGCTGTCGCCAGAAATCCCTTCATGCC 1521

RESULT 8  
 ACC47594  
 ID ACC47594 standard; cDNA; 222 BP.  
 XX  
 AC ACC47594;  
 XX  
 DT 23-JUN-2003 (first entry)  
 XX  
 DE Disintegrin-gamma cDNA, SEQ ID NO:3.  
 XX  
 KW Disintegrin-gamma; cysteine-rich; RGD motif; integrin antagonist;  
 KW inhibition; vascularisation; tumour growth; tumour metastasis; cancer;  
 KW cytoskeletal; gene; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..222  
 FT /\*tag= a  
 FT /partial  
 FT /product= "Disintegrin-gamma"  
 FT /note= "No start codon given in the specification"  
 FT /transl\_except= (pos:16..18, aa:Tyr)  
 FT /transl\_except= (pos:46..48, aa:Tyr)  
 FT /transl\_except= (pos:124..126, aa:Gln)  
 FT /transl\_except= (pos:127..129, aa:Gln)  
 FT /note= "The above translation exceptions relate only to  
 FT the version of disintegrin-gamma shown in ABP97447)"  
 XX  
 PN CN1374318-A.  
 XX  
 PD 16-OCT-2002.  
 XX  
 PF 08-FEB-2002; 2002CN-00103679.  
 XX  
 PR 08-FEB-2002; 2002CN-00103679.  
 XX  
 PA (MIU/) MI J.  
 XX  
 PI MI J;

```
XX WPI: 2003-168400/17.
DR P-PSDB; ABB97447, ABB97448.
XX
XX New natural dissociation essence gamma gene and antileoplastic active
PT polypeptide dissociation essence-gamma, useful as a fusion body
PT antagonist to inhibit vascularization, tumor metastasis and tumor growth.
XX
XX Claim 1; Page 7 (Disclosure); 12pp; Chinese.
XX
XX The invention relates to a disintegrin-gamma protein (ABB97447, ABB97448)
CC and nucleic acids encoding it (ACC47594). Disintegrin-gamma is cysteine-
CC rich, contains an RGD integrin-binding motif, and acts as an integrin
CC antagonist. Disintegrin gamma may be used to inhibit integrin-mediated
CC activities such as vascularization, and tumor growth and metastasis. The
CC present sequence represents cDNA encoding disintegrin-gamma
XX
SQ Sequence 222 BP; 67 A; 49 C; 62 G; 44 T; 0 U; 0 Other;
Query Match 82.0%; Score 174.6; DB 8; Length 222;
Best Local Similarity 88.7%; Pred. No. 2.2e-49;
Matches 189; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GGAAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTCCTCGATGCTGCAACTGTAA 60
DB 7 GGAAGAAGATGTGACTGTGGCGCTCTCTGCAATCCGTCCTCGATGCTGCAACTGTAA 66
QY 61 CTGAGACCAAGGCGGCGCACTGTGACAGAGACTGTGTGACCACTGCAAGTTATGAAA 120
DB 67 CTGAACCAAGAGGACGACGTGTACAGAGACCGGCTGTGTGACCAAGGCGCAAGTTAAAGAA 126
QY 121 GAAGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGATA 180
DB 127 GAAGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGATA 186
QY 181 TCTGCTGCTGTCCCGAAGATCCCTTCATGCGC 213
DB 187 TCTGCTGCTGTCCCGAAGATCCCTTCATGCGC 219
RESULT 9
AAQ50357
ID AAQ50357 standard; cDNA; 174 BP.
XX
XX AAQ50357;
AC
XX 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE pAgalphi201 platelet aggregation inhibitory polypeptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydinus halye blomhoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI: 1993-348481/44.
XX
XX P-PSDB; AAR42887.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
PT platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Fig 3; 50pp; Japanese.
PS
```

```
XX The sequence is that of pAgalphi201 cDNA which comprises a polypeptide
CC isolated from Agkistrodon halye blomhoffi. It was used in the isolation
CC and prodn. of a polypeptide inhibiting platelet aggregation caused by
CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 174 BP; 50 A; 31 C; 55 G; 38 T; 0 U; 0 Other;
Query Match 72.7%; Score 154.8; DB 2; Length 174;
Best Local Similarity 93.1%; Pred. No. 1.2e-42;
Matches 162; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4 GAGAAATGTACTGTGGCGCTCTCTGCAATCCGTCCTCGATGCTGCAACTGTAAACTG 63
DB 1 GAGAACTGGACTGTGGCGCTCTCTGCAATCCGTCCTGTGATGCTGCAACTGTAAACTG 60
QY 64 AGACCAAGGCGCCAGTGTGACAGAGACTGTGTGTGACCACTGCAAGTTATGAAAAGAA 123
DB 61 AGACCAAGGCGCACTGTGACAGAGAGACTGTGTGTGACCACTGCAAGTTATGAAAAGAA 120
QY 124 GGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGC 177
DB 121 GGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGC 174
RESULT 10
AAQ44933
ID AAQ44933 standard; cDNA; 174 BP.
XX
XX AAQ44933;
AC
XX 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE pAgalphi2-101 platelet aggregation inhibitory polypeptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydinus halye blomhoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI: 1993-348481/44.
XX
XX P-PSDB; AAR46947.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
PT platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Fig 13; 50pp; Japanese.
XX
XX The sequence is that of pAgalphi2-101 cDNA which comprises a polypeptide
CC isolated from Agkistrodon halye blomhoffi. It was used in the isolation
CC and prodn. of a polypeptide inhibiting platelet aggregation caused by
CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 174 BP; 51 A; 31 C; 55 G; 37 T; 0 U; 0 Other;
Query Match 71.9%; Score 153.2; DB 2; Length 174;
Best Local Similarity 92.5%; Pred. No. 4.2e-42;
Matches 161; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 4 GAAAGATGTACTGTGGCGCTCTCTGCAATCCGTCCTCGATGCTGCAACTGTAAACTG 63
```

Db 1 GAGGACTGCGACTGTGCTCTCTGGAATCCGGTGTGATGCTGTGCACTGTAACCTG 60  
QY 64 AGACCAAGGCGGCGAGTGTGCAAGAGCACTGTGTGACCAAGTGCAGATTATGAAGAA 123  
Db 61 AGACCAAGGCGAGCACTGTGTGCAAGAGCACTGTGTGTGACCAAGTGCAGATTATGAAGAAAA 120  
QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177  
Db 121 GGAACAGTATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

## RESULT 11

AAQ50385  
ID AAQ50385 standard; cDNA to mRNA; 174 BP.

AC AAQ50385;

DT 24-OCT-2003 (revised)  
DT 11-MAY-1994 (first entry)

DE Platelet aggregation inhibitory peptide.

KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.

OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

PF 03-OCT-1991; 91JP-00256234.

PR 26-OCT-1990; 90JP-00287116.

PR 20-FEB-1991; 91JP-00026328.

PA (TAKE ) TAKEDA CHEM IND LTD.

DR WPI; 1993-348481/44.

DR P-PSDB; AAR42858.

PT Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.

PS Example; Page 27; 50pp; Japanese.

CC The sequence is that encoding a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.

CC (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 174 BP; 51 A; 31 C; 55 G; 37 T; 0 U; 0 Other;

Query Match 71.9%; Score 153.2; DB 2; Length 174;

Best Local Similarity 92.5%; Pred. No. 4.2e-42; Matches 161; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 GAAAGATGTAAGTGTGGGCTCTGCAAAATCCGTGCTGCAATGCTGCAACCTGTAACTG 63  
Db 1 GAGGACTGCGACTGTGCTCTCTGGAATCCGGTGTGATGCTGTGCACTGTAACCTG 60  
QY 64 AGACCAAGGCGGCGAGTGTGCAAGAGCACTGTGTGACCAAGTGCAGATTATGAAGAA 123  
Db 61 AGACCAAGGCGAGCACTGTGTGCAAGAGCACTGTGTGTGACCAAGTGCAGATTATGAAGAAAA 120  
QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177  
Db 121 GGAACAGTATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

## RESULT 12

AAQ44932  
ID AAQ44932 standard; cDNA; 174 BP.

XX

AC AAQ44932;  
XX 24-OCT-2003 (revised)  
DT 11-MAY-1994 (first entry)

DE pAgalphi-101 platelet aggregation inhibitory polypeptide.

KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.

OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

PF 03-OCT-1991; 91JP-00256234.

PR 26-OCT-1990; 90JP-00287116.

PR 20-FEB-1991; 91JP-00026328.

PA (TAKE ) TAKEDA CHEM IND LTD.

DR WPI; 1993-348481/44.

DR P-PSDB; AAR46946.

PT Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.

PS Example; Fig 12; 50pp; Japanese.

CC The sequence is that of pAgalphi-101 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by

CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 174 BP; 50 A; 31 C; 54 G; 39 T; 0 U; 0 Other;

Query Match 71.2%; Score 151.6; DB 2; Length 174;

Best Local Similarity 92.0%; Pred. No. 1.5e-41; Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GAAAGATGTAAGTGTGGGCTCTGCAAAATCCGTGCTGCAATGCTGCAACCTGTAACTG 63  
Db 1 GAGGACTGCGACTGTGCTCTCTGGAATCCGGTGTGATGCTGTGCACTGTAACCTG 60  
QY 64 AGACCAAGGCGGCGAGTGTGCAAGAGCACTGTGTGACCAAGTGCAGATTATGAAGAA 123  
Db 61 AGACCAAGGCGAGCACTGTGTGCAAGAGCACTGTGTGTGACCAAGTGCAGATTATGAAGAAAA 120  
QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177  
Db 121 GGAACAGTATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

## RESULT 13

AAQ50390  
ID AAQ50390 standard; cDNA to mRNA; 174 BP.

XX AAQ50390;

DT 24-OCT-2003 (revised)

DT 11-MAY-1994 (first entry)

DE Platelet aggregation inhibitory peptide.

KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.

OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

XX 03-OCT-1991; 91JP-00256234.  
XX 26-OCT-1990; 90JP-00287116.  
XX 20-FEB-1991; 91JP-00026328.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX WPI; 1993-348481/44.  
XX P-PSDB; AAR42863.  
XX Polypeptide of specified aminoacid sequence - used for inhibiting  
XX platelet aggregation caused by e.g. collagen, thrombin, etc.  
XX Example; Page 30; 50pp; Japanese.  
XX The sequence is that encoding a polypeptide which inhibits platelet  
XX aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.  
XX (Updated on 24-OCT-2003 to standardise OS field)  
XX Sequence 174 BP; 50 A; 32 C; 55 G; 37 T; 0 U; 0 Other;  
SQ

Query Match 71.2%; Score 151.6; DB 2; Length 174;  
Best Local Similarity 92.0%; Pred. No. 1.5e-41;  
Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAACTG 63  
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGATGCTGCAACCTGTAACTG 60  
QY 64 AGACCAAGGCGCGCACTGTGCAAGAGACTGTGTCACCGATGCAATTTATGAAGA 123  
DB 61 AGACCAAGAGCAAGCTGTGCAAGAGACTGTGTCACCGATGCAATTTATGAAGA 120  
QY 124 GAACATATATGCGCGATGCGCAAGGGGTATGATGATGATTAATCTGCAATGCG 177  
DB 121 GGAACAGTATGCGGATAGCAAGGGGTATGATGATGATTAATCTGCAATGCG 174

RESULT 14  
AAQ50384  
ID AAQ50384 standard; cDNA to mRNA; 174 BP.  
XX  
XX AAQ50384;  
AC 24-OCT-2003 (revised)  
XX 11-MAY-1994 (first entry)  
DT  
XX Platelet aggregation inhibitory peptide.  
DE  
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.  
XX  
XX Gloydins hays blomhoffi.  
OS  
XX JP05255395-A.  
XX 05-OCT-1993.  
XX 03-OCT-1991; 91JP-00256234.  
XX 26-OCT-1990; 90JP-00287116.  
XX 20-FEB-1991; 91JP-00026328.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX WPI; 1993-348481/44.  
XX P-PSDB; AAR42857.  
XX Polypeptide of specified aminoacid sequence - used for inhibiting  
XX platelet aggregation caused by e.g. collagen, thrombin, etc.  
XX Example; Page 27; 50pp; Japanese.

CC The sequence is that encoding a polypeptide which inhibits platelet  
CC aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.  
CC (Updated on 24-OCT-2003 to standardise OS field)  
XX  
XX Sequence 174 BP; 50 A; 31 C; 54 G; 39 T; 0 U; 0 Other;  
SQ

Query Match 71.2%; Score 151.6; DB 2; Length 174;  
Best Local Similarity 92.0%; Pred. No. 1.5e-41;  
Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAACTG 63  
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGATGCTGCAACCTGTAACTG 60  
QY 64 AGACCAAGGCGCGCACTGTGCAAGAGACTGTGTCACCGATGCAATTTATGAAGA 123  
DB 61 AGACCAAGAGCAAGCTGTGCAAGAGACTGTGTCACCGATGCAATTTATGAAGA 120  
QY 124 GAACATATATGCGCGATGCGCAAGGGGTATGATGATGATTAATCTGCAATGCG 177  
DB 121 GGAACAGTATGCGGATAGCAAGGGGTATGATGATGATTAATCTGCAATGCG 174

RESULT 15  
AAQ4934  
ID AAQ4934 standard; cDNA; 174 BP.  
XX  
XX AAQ4934;  
AC 24-OCT-2003 (revised)  
XX 11-MAY-1994 (first entry)  
DT  
XX pAgalpa3-101 platelet aggregation inhibitory polypeptide.  
DE  
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.  
XX Gloydins hays blomhoffi.  
OS  
XX JP05255395-A.  
XX 05-OCT-1993.  
XX 03-OCT-1991; 91JP-00256234.  
XX 26-OCT-1990; 90JP-00287116.  
XX 20-FEB-1991; 91JP-00026328.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX WPI; 1993-348481/44.  
XX P-PSDB; AAR46948.  
XX Polypeptide of specified aminoacid sequence - used for inhibiting  
XX platelet aggregation caused by e.g. collagen, thrombin, etc.  
XX Example; Fig 14; 50pp; Japanese.  
XX The sequence is that of pAgalpa3-101 cDNA which comprises a polypeptide  
XX isolated from Agkistrodon hays blomhoffi. It was used in the isolation  
XX and prodn. of a polypeptide inhibiting platelet aggregation caused by  
XX ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-  
XX 2003 to standardise OS field)  
SQ Sequence 174 BP; 49 A; 32 C; 54 G; 39 T; 0 U; 0 Other;

Query Match 70.4%; Score 150; DB 2; Length 174;  
Best Local Similarity 91.4%; Pred. No. 5.2e-41;  
Matches 159; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAACTG 63  
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGATGCTGCAACCTGTAACTG 60



QY 64 AGACCAAGGCGCGCACTGTGTGCAAGAAAGACTGTGTGTGACAGTGCAGATTTATGAAGAA 123  
DB 61 AGACAAAGAGCACAAGTGTGTGCAAGAAAGACTGTGTGTGACAGTGCAGATTTTAAAAAA 120  
QY 124 GAAACATATGCGCGATGCAAGGGGTGATGACATGGATGATTACTGCAATGGC 177  
DB 121 GAAACATATGCGCGATGCAAGGGGTGATGACATGGATGATTACTGCAATGGC 174

Search completed: December 3, 2004, 18:47:15  
Job time : 409 secs

**This Page Blank (uspio)**

; Sequence 1, Application US/09460295B

Patent No. 6710030  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
TITLE OF INVENTION: CONTORESTININ (CN) AND METHODS FOR ITS USE IN PREVENTING METAST  
FILE REFERENCE: 1279-338C3/09801388  
CURRENT APPLICATION NUMBER: US/09/460,295B  
CURRENT FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 09/163,047  
PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent version 3.1  
SEQ ID NO 1  
LENGTH: 2029  
TYPE: DNA  
ORGANISM: Agkistrodon contortrix  
US-09-460-295B-1

Query Match 89.5%; Score 190.6; DB 4; Length 2029;  
Best Local Similarity 93.4%; Pred. No. 8.8e-56;  
Matches 199; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGAGAGAATGATGCTGGCGCTCCGCAATCCGTCGATGCTGCAACCTGTAAA 60  
DB 1323 GGAGAGAATGATGCTGGCGCTCCGCAATCCGTCGATGCTGCAACCTGTAAA 1382

QY 6T CTGAGACCGAGGGCGCAGCTGTGCAAGAGACTGTGTGTGACAGTCCAGATTATGAAA 120  
DB 1383 CTGACACAGAGGTACAGATGTGACAGATGACTGTGTGTGACAGTCCAGATTATGAAA 1442

QY 121 GAAGAACATATGCGGATGCGAAGGGGTGATGACATGATGATGCTGCAATGGCATA 180  
DB 1443 GAAGAACATATGCGGATGCGAAGGGGTGATGACATGATGATGCTGCAATGGCATA 1502

QY 181 TCTGCTGCTGCTCCGAGAAATCCCTTCATGCC 213  
DB 1503 TCTGCTGCTGCTCCGAGAAATCCCTTCATGCC 1535

RESULT 3  
US-08-745-603-1  
Sequence 1, Application US/08745603  
Patent No. 5814609  
GENERAL INFORMATION:  
APPLICANT: Francis S. Markland, Jr.  
TITLE OF INVENTION: COMPOSITIONS CONTAINING A DISINTEGRIN AND METHODS FOR  
TITLE OF INVENTION: ITS USE IN PREVENTING METASTASIS AND OTHER CONDITIONS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berlin & Carson  
STREET: 201 No. 5814609th Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: ASCII DOS/TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/745,603  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert Berlin  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 1920-338C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213/977-1001  
TELEFAX: 213/977-1003  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 911 base pairs (111 amino acids)  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-745-603-1

Query Match 78.4%; Score 167; DB 1; Length 911;  
Best Local Similarity 94.5%; Pred. No. 8.4e-48;  
Matches 173; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 31 AATCCGTGCTGCATGCTGCAACCTGTAACTGAGACCGAGGCGCATGTGCAAGAGA 90  
DB 235 AATCCGTGCTGCATGCTGCAACCTGTAACTGAGACCGAGGCGCATGTGCAAGAGA 294

QY 91 CTGTGTGACCACTGACAGATTATGAAAGAAAGAAATATGCGGATGCGAAGGCT 150  
DB 295 CTGTGTGACCACTGACAGATTATGAAAGAAAGAAATATGCGGATGCGAAGGCT 354

QY 151 GATGACATGATGATTAATGCAATGCAATATCTGCTGCTGCTCCAGAAATCCCTTCAT 210  
DB 355 GATGACATGATGATTAATGCAATGCAATATCTGCTGCTGCTCCAGAAATCCCTTCAT 414

QY 211 GCC 213  
DB 415 GCC 417

RESULT 4  
5182260-22  
Patent No. 5182260  
APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.  
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM  
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING  
THOSE INHIBITORS AND COMPOSITIONS USING THEM  
NUMBER OF SEQUENCES: 22  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,313  
FILING DATE: 01-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 303,585  
FILING DATE: 27-JAN-1989  
APPLICATION NUMBER: 303,590  
FILING DATE: 27-JAN-1989  
SEQ ID NO: 22  
LENGTH: 219  
5182260-22

Query Match 59.1%; Score 125.8; DB 6; Length 219;  
Best Local Similarity 75.1%; Pred. No. 7.1e-34;  
Matches 157; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGAGAGAATGATGCTGGCGCTCCGCAATCCGTCGATGCTGCAACCTGTAAA 60  
DB 10 GGAGAGAATGATGCTGGCGCTCCGCAATCCGTCGATGCTGCAACCTGTAAA 69

QY 61 CTGAGACCGAGGGCGCAGCTGTGCAAGAGACTGTGTGCAAGTGAATTATGAAA 120  
DB 70 CTGAGACCGAGGGCGCAGCTGTGCAAGAGACTGTGTGCAAGTGAATTATGAAA 129

QY 121 GAAGAACATATGCGGATGCGAAGGGGTGATGACATGATGATGCTGCAATGGCATA 180  
DB 130 GAAGAACATATGCGGATGCGAAGGGGTGATGACATGATGATGCTGCAATGGCATA 189

QY 181 TCTGCTGCTGCTCCGAGAAATCCCTTCGA 209  
DB 190 TCTGCTGCTGCTCCGAGAAATCCCTTCGA 218

RESULT 5  
5182260-1

Patent No. 5182260  
APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.  
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM  
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING  
THOSE INHIBITORS AND COMPOSITIONS USING THEM  
NUMBER OF SEQUENCES: 22  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,313  
FILING DATE: 01-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 303,585  
FILING DATE: 27-JAN-1989  
APPLICATION NUMBER: 303,590  
FILING DATE: 27-JAN-1989  
SEQ ID NO: 1:  
LENGTH: 226  
5182260-1  
Query Match 59.1%; Score 125.8; DB 6; Length 226;  
Best Local Similarity 75.1%; Pred. No. 7.2e-34;  
Matches 157; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 1 GGAGAAAGATGTGACTGTGGGCGCTCCGCAAAATCCGCTGCGATGCTGCAACCTGTAA 60  
DB 11 GGTGAAGATGCGACTGCGATCCCGGAAAACCCGCTGCGACGCGGCCACTGCGAA 70  
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCACTGCGATTATGAA 120  
DB 71 CTGCTCGCGGTGACAGTGTGCAAGAGGCTGTGCTGCGACACAGTGCATTCAGAA 130  
QY 121 GAAGAAACAATATCCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGCAT 180  
DB 131 GAAGTACCGTTTCCGCTGCTGCTGAGGTGACGACGTTAAGACTTACGAAAGTATC 190  
QY 181 TCTGCTGCTGTCCGAGAAATCCCTTCCA 209  
DB 191 TCTGAGGTGCGCCGCGTAACCCGTTCCA 219  
RESULT 6  
US-07-623-611-11  
Sequence 11, Application US/07623611  
Patent No. 5242810  
GENERAL INFORMATION:  
APPLICANT: Maraganore, John M.  
APPLICANT: Chao, Betty H.  
APPLICANT: Strauch, Kathryn L.  
APPLICANT: Thompson, Jeffrey S.  
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue - 29th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/623,611  
FILING DATE: 19901207  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: N  
ANTI-SENSE: N  
US-07-623-611-11  
Query Match 56.3%; Score 120; DB 1; Length 288;  
Best Local Similarity 72.5%; Pred. No. 8.1e-32;  
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;  
QY 1 GGAGAAAGATGTGACTGTGGGCGCTCCGCAAAATCCGCTGCGATGCTGCAACCTGTAA 60  
DB 7 GGTGAAGATGCGACTGCGATCCCGGAAAACCCGCTGCGACGCGCTGCTGCAATC 66  
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCACTGCGATTATGAA 120  
DB 67 CTGCTCGCGGTGCTGAGTGTGCAAGGCTGTGCTGCGACAGTGCATTCAGAA 126  
QY 121 GAAGAAACAATATCCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGCAT 180  
DB 127 GAAGTACCGTTTCCGCTGCTGCTGAGGTGACGACGTTAAGACTTACGAAAGTATC 186  
QY 181 TCTGCTGCTGTCCGAGAAATCCCTTCCATG 211  
DB 187 TCTGAGGTGCGCCGCGTAACCCGTTCCA 217  
RESULT 7  
PCT-US91-09108-11  
Sequence 11, Application PC/TUS9109108  
GENERAL INFORMATION:  
APPLICANT: Biogen, Inc.  
TITLE OF INVENTION: \*', BIFUNCTIONAL INHIBITORS OF THROMBIN ANDPLATELET ACTIVAT  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue - 29th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/09108  
FILING DATE: 19911205  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600  
TELEFAX: (212) 715-0674  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: N

ANTI-SENSE: N  
PCT-US91-09108-11

Query Match 56.3%; Score 120; DB 5; Length 288;  
Best Local Similarity 72.5%; Pred. No. 8.1e-32;  
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATCTGAGCGCTCCCTGCAAAATCCGTCGCGAGTGTGCAACCTGTAAA 60  
DB 7 GGTAAGAAATGTGATCTGAGCGATCCCGAAAAACCGTGCACGACGCTGCTACCTGCAAA 66  
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCAAGTGCAGATTATGAAA 120  
DB 67 CTGCGTCCGGGTGCTCACTGCGGTGAAGTCTGTGTCGACCAAGTGCAGATTATGAAA 126  
QY 121 GAAGAAACAATATGCGCGATGCGCAAGGGGTATACATGATGATTTACTGCAATGCGATA 180  
DB 127 GAAGGTACCGTTTGGCGGTGCTGTGTGACGACGTAAACGACTACTGCAACGGTATC 186  
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATG 211  
DB 187 TCTGAGGTTCGCCCGCGTAACCGCTTCACG 217

RESULT 8  
US-07-623-611-10  
Sequence 10, Application US/07623611

Patent No. 5242810

GENERAL INFORMATION:

APPLICANT: Maraganore, John M.

APPLICANT: Chao, Betty H.

APPLICANT: Strauch, Kathryn L.

APPLICANT: Thompson, Jeffrey S.

TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND

TITLE OF INVENTION: PLATELET ACTIVATION

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 875 Third Avenue - 29th Floor

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/623,611

FILING DATE: 19901207

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

US-07-623-611-10

Query Match 56.2%; Score 119.6; DB 1; Length 288;  
Best Local Similarity 72.7%; Pred. No. 1.1e-31;

Matches 152; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATCTGAGCGCTCCCTGCAAAATCCGTCGCGAGTGTGCAACCTGTAAA 60  
DB 79 GGTAAGAAATGTGATCTGAGCGATCCCGAAAAACCGTGCACGACGCTGCTACCTGCAAA 138  
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCAAGTGCAGATTATGAAA 120  
DB 139 CTGCGTCCGGGTGCTCACTGCGGTGAAGTCTGTGTCGACCAAGTGCAGATTATGAAA 198  
QY 121 GAAGAAACAATATGCGCGATGCGCAAGGGGTATACATGATGATTTACTGCAATGCGATA 180  
DB 199 GAAGGTACCGTTTGGCGGTGCTGTGTGACGACGTAAACGACTACTGCAACGGTATC 258  
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCGA 209  
DB 259 TCTGAGGTTCGCCCGCGTAACCGCTTCGA 287

RESULT 9  
PCT-US91-09108-10

Sequence 10, Application PC/TUS9109108

GENERAL INFORMATION:

APPLICANT: Biogen, Inc.

TITLE OF INVENTION: \*\", BIFUNCTIONAL INHIBITORS OF THROMBIN AND PLATELET ACTIVAT

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 875 Third Avenue - 29th Floor

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/09108

FILING DATE: 19911205

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

PCT-US91-09108-10

Query Match 56.2%; Score 119.6; DB 5; Length 288;  
Best Local Similarity 72.7%; Pred. No. 1.1e-31;  
Matches 152; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATCTGAGCGCTCCCTGCAAAATCCGTCGCGAGTGTGCAACCTGTAAA 60  
DB 79 GGTAAGAAATGTGATCTGAGCGATCCCGAAAAACCGTGCACGACGCTGCTACCTGCAAA 138  
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCAAGTGCAGATTATGAAA 120  
DB 139 CTGCGTCCGGGTGCTCACTGCGGTGAAGTCTGTGTCGACCAAGTGCAGATTATGAAA 198



NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,001A  
FILING DATE: 18-FEB-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15293B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 78..1940  
US-09-026-001A-5

Query Match 41.8%; Score 89; DB 4; Length 2050;  
Best Local Similarity 69.7%; Pred. No. 9.9e-21;  
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

QY 1 GGAGGAAGATGTGACTGTGGCGCTCTCG-----CAATCGGTGCTGCATGCTGCA 51  
DB 1332 GGAGGAAGATGTGACTGTGGCGCTCTCTCGAGATTGTCAAAATACCTGCTGTGATGCTGCA 1391

QY 52 ACCGTAAACTGAGACCAAGGGGCGAGTGTGCAGAGAAGACTGTGTGACCACTGAGA 111  
DB 1392 ACTTGTAACTGCAACATGAGGACAGTGTACTGTGAGAGTGTGTGAGAAATGCAAA 1451

QY 112 TTATGAAGAAGAGACATATGCCGATGCGCAAGGGGTGA---TGAATGATGATTAC 168  
DB 1452 TTAAAGGAGGAGGAGGAGATGCCGGGCGAGCAAAAGATGACTGTGACTTCTGAACTC 1511

QY 169 TGCATGGCATATCTGCTGCGCTGCTCCCAAGAAATCCCTTCCA 209  
DB 1512 TGCATGGCGCATCTGCTGTAAGTGTCCCAAGACAGCTTCCA 1552

RESULT 14  
US-09-026-001A-9  
Sequence 9, Application US/09026001A  
Patent No. 6413760  
GENERAL INFORMATION:  
APPLICANT: Boonhoo, Amechand  
APPLICANT: Seehra, Jasbir  
APPLICANT: Shaw, Gray  
APPLICANT: Sako, Dianne  
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,001A  
FILING DATE: 18-FEB-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15293B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-026-001A-9

Query Match 41.8%; Score 89; DB 4; Length 2335;  
Best Local Similarity 69.7%; Pred. No. 1.1e-20;  
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

QY 1 GGAGGAAGATGTGACTGTGGCGCTCTCG-----AAATCGGTGCTGCATGCTGCA 51  
DB 1321 GGAGGAAGATGTGACTGTGGCGCTCTCTCGGATTGTCAAAGTCTGTGGAAGCTTCA 1380

QY 52 ACCGTAAACTGAGACCAAGGGGCGAGTGTGCAGAGAAGACTGTGTGACCACTGAGA 111  
DB 1381 ACTTGTAACTGCAACATCTCATGACAGTGTACTCCGAAGGCTGTGTGAGAAATGCAAA 1440

QY 112 TTATGAAGAAGAGACATATGCCGATGCGCAAGGGGTGA---TGAATGATGATTAC 168  
DB 1441 TTAAAGGAGGAGGAGGAGATGCCGGGCGAGCAAAAGATGACTGTGACTTCTGAACTC 1500

QY 169 TGCATGGCATATCTGCTGCGCTGCTCCCAAGAAATCCCTTCCA 209  
DB 1501 TGCATGGCGCATCTGCTGTAAGTGTCCCAAGACAGCTTCCA 1541

RESULT 15  
US-09-026-001A-17  
Sequence 17, Application US/09026001A  
Patent No. 6413760  
GENERAL INFORMATION:  
APPLICANT: Boonhoo, Amechand  
APPLICANT: Seehra, Jasbir  
APPLICANT: Shaw, Gray  
APPLICANT: Sako, Dianne  
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-026-001A-17

```

```

Query Match 41.8%; Score 89; DB 4; Length 2359;
Best Local Similarity 69.7%; Pred. No. 1,1e-20;
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

```

```

QY 1 GGAGAGAGATGTGACTGTGGCGCTTCCTGC-----AAATCGGTGCTGCGATGCTGCA 51
    |||
DB 1345 GGAGAGAGATGTGACTGTGGCGCTTCCTGCAGATTGTCAAGTGTCTGCGAGCTPACA 1404
    |||
QY 52 ACCTGTAACTGAGACCGAGGCGCAGTGTGCAGAGAGACTGTGTGTGACCAAGTGCGAGA 111
    |||
DB 1405 ACTGTAACTGACACACCTCATGCAAGTGTGACTCCGAGGGTGTGTGAGAAATGCAAA 1464
    |||
QY 112 TTATGAAAGAGAGACATATGCCGATGCGAAGGGGTGA---TGACATGATGATTAC 168
    |||
DB 1465 TTTAAGGAGAGAGAGAGATGCGGGGCAAGAGATGCTGTGACTTGCTGAACTC 1524
    |||
QY 169 TGCATGCGCATATCTGCTGGCTGTCCCAAGAAATCCCTTCCA 209
    |||
DB 1525 TGCACTGGCCCATCTGCTGAGTGTCCCAAGACATCTTCCA 1565
    |||

```

Search completed: December 3, 2004, 20:10:12  
 Job time : 90 secs

This Page Blank (uspio)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:11:26 ; Search time 2974 Seconds  
(without alignments)  
2609,840 Million cell updates/sec

Title: US-10-089-473a-2

Perfect score: 213  
Sequence: 1 ggagaagaatgtgactgtg.....ccagaatccctccatgc 213

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc1:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182.6	85.7	409	4	EM401624 JLD07F S
2	180.6	84.8	399	4	EM401419 GH063F S
3	101.2	47.5	476	4	EM401547 JH012F S
4	100.4	47.1	444	4	EM401444 JH1A04F S
5	100.2	47.0	357	4	EM401492 JH2B04F S
6	100.2	47.0	432	4	EM401556 JH3F08F S
7	98.2	46.1	377	4	EM401456 JH1C08F S
8	74.6	35.0	420	4	EM401655 JLD203F S
9	68.2	32.0	411	4	EM401433 GH089F S
10	68.2	32.0	474	4	EM401391 GH010F S
11	68.2	32.0	527	4	EM401397 GH020F S
12	68.2	32.0	542	4	EM401405 GH029F S
13	68.2	32.0	565	4	EM401393 GH016F S
14	60.6	28.5	845	7	CF377167 AGENCOURT
15	60.6	28.5	863	7	A1525705 PT1.3_04_
16	58.4	27.4	519	1	AL783368 AL783368
17	55.6	26.1	384	1	EM401619 JH1C10F S
18	54.8	25.7	846	7	CK596457 AGENCOURT
19	54	25.4	395	1	AA280392 Z10404.r
20	54	25.4	593	6	CD535662 Leukoms.7
21	52.4	24.6	549	2	BE389727 601281979
22	52.4	24.6	603	2	BE388922 601282620
23	52.4	24.6	635	2	BE388453 601285592
24	52.4	24.6	706	2	BE389752 601282919

25	52.4	24.6	968	2	BE410120 601302417
26	52.4	24.6	3108	3	AF326918 Homo sapi
27	51.2	24.0	572	2	BE390985 601283174
28	50.4	23.7	620	5	BX670023 BX670023
29	50.4	23.7	690	5	BX670024 BX670024
30	50.4	23.7	852	6	CD361846 AGENCOURT
31	48.8	22.9	366	4	BG000250 MR3-GN022
32	48.8	22.9	643	4	BM538117 ha90d11.9
33	48.4	22.7	955	5	BX336226 BX336226
34	47.8	22.4	707	1	AU136809 AU136809
35	47.6	22.3	450	2	AM605922 RCI-HT025
36	47.4	22.3	727	1	AU127125 AU127125
37	47.2	22.2	335	2	BF771395 IL5-IT002
38	47.2	22.2	340	1	AA368597 EST60160
39	47.2	22.2	362	5	BQ368056 QV0-GN014
40	47.2	22.2	375	1	AA368827 EST60139
41	47.2	22.2	383	4	BF987229 QV0-GN014
42	47.2	22.2	388	6	CI8735 CI8735 Huma
43	47.2	22.2	401	5	BQ367967 PM4-GN051
44	47.2	22.2	404	4	BG012562 IL5-GN023
45	47.2	22.2	411	7	T54209 Ya30c07.12

## ALIGNMENTS

RESULT 1  
EM401624 409 bp mRNA linear EST 01-MAY-2002  
JLD07F Snake Bothrops insularis library IL3 Bothrops insularis  
LOCUS  
DEFINITION  
CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.  
EM401624  
ACCESSION  
EM401624.1 GI:20376252  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Bothrops insularis (Island Jararaca)  
Bothrops insularis  
Lepidocrypta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.  
1 (bases 1 to 409)

REFERENCE  
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)  
Tunqueira-de-Azevedo, I.L.M. and Ho, P.L.  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hopie@usp.br  
This EST corresponds to cluster BTM08A (see Reference)  
Seq primer: M13F.  
Location/Qualifiers  
1..409

CONTACT: Paulo Lee HO  
Centro de Biotecnologia  
Instituto Butantan  
Av. Vital Brasil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hopie@usp.br  
This EST corresponds to cluster BTM08A (see Reference)  
Seq primer: M13F.  
Location/Qualifiers  
1..409

FEATURES  
source  
/organism="Bothrops insularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8723"  
/feature\_type="venom glands"  
/clone\_lib="Snake Bothrops insularis library IL3"  
/note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco R1; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco R1 adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or

## ORIGIN

cluster was obtained through Blast searches (e-value < e-05)."

Query Match 85.7%; Score 182.6; DB 4; Length 409;  
Best Local Similarity 91.1%; Pred. No. 1.2e-45;  
Matches 194; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 60  
DB 85 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 144  
QY 61 CTGAGACCAAGGCGCCAGTGTGACAGAGACTGTGTGTGACAGTGCAGATTATGAAA 120  
DB 145 CTGAGACCAAGGCGCCAGTGTGACAGAGACTGTGTGTGACAGTGCAGATTATGAAA 204  
QY 121 GAAGAACCAATATGCGCGAGTGCAGAGGGGTATGACATGATGATTAATCTGCATGSCATA 180  
DB 205 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 264  
QY 181 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 213  
DB 265 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 297

RESULT 2  
BM401419 399 bp mRNA linear EST 01-MAY-2002  
LOCUS BM401419  
DEFINITION GH063P Snake Bothrops insularis library IL2 Bothrops insularis cDNA  
5' similar to Snake venom metalloproteinase, mRNA sequence.  
ACCESSION BM401419.1 GI:20376047  
VERSION BM401419.1  
KEYWORDS EST.  
SOURCE Bothrops insularis (Island Jararaca)  
ORGANISM Bothrops insularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.

REFERENCE  
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)  
JOURNAL Gene 289 (1-2), 279-291 (2002)  
MEDLINE 22347338  
PUBMED 12459276

COMMENT  
Contact: Paulo Lee Ho  
Centro de Biotecnologia  
Instituto Butantan  
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hoplee@usp.br  
This EST corresponds to cluster BITW08A (see Reference)  
Seq primer: M13F.

FEATURES  
source 1..399  
Location/Qualifiers

/organism="Bothrops insularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8723"  
/tissue\_type="venom glands"  
/clone\_lib="Snake Bothrops insularis library IL2"  
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <

## ORIGIN

e-05)."

Query Match 84.8%; Score 180.6; DB 4; Length 399;  
Best Local Similarity 90.1%; Pred. No. 5e-45;  
Matches 192; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 60  
DB 108 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 167  
QY 61 CTGAGACCAAGGCGCCAGTGTGACAGAGACTGTGTGTGACAGTGCAGATTATGAAA 120  
DB 168 CTGAGACCAAGGCGCCAGTGTGACAGAGACTGTGTGTGACAGTGCAGATTATGAAA 227  
QY 121 GAAGAACCAATATGCGCGAGTGCAGAGGGGTATGACATGATGATTAATCTGCATGSCATA 180  
DB 228 GGAGAAAGATGTGATCTGTGGCGCTCTTCCAAATCCGTCGCACTGTGAAA 287  
QY 181 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 213  
DB 288 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 320

RESULT 3  
BM401547 476 bp mRNA linear EST 01-MAY-2002  
LOCUS BM401547  
DEFINITION JH3D12P Snake Bothrops insularis library IL3 Bothrops insularis  
cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.  
ACCESSION BM401547.1 GI:20376175  
VERSION BM401547.1  
KEYWORDS EST.  
SOURCE Bothrops insularis (Island Jararaca)  
ORGANISM Bothrops insularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.

REFERENCE  
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)  
JOURNAL Gene 289 (1-2), 279-291 (2002)  
MEDLINE 22347338  
PUBMED 12459276

COMMENT  
Contact: Paulo Lee Ho  
Centro de Biotecnologia  
Instituto Butantan  
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hoplee@usp.br  
This EST corresponds to cluster BITW06A (see Reference)  
Seq primer: M13F.

FEATURES  
source 1..476  
Location/Qualifiers

/organism="Bothrops insularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8723"  
/tissue\_type="venom glands"  
/clone\_lib="Snake Bothrops insularis library IL3"  
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <

## ORIGIN

Query Match 47.5%; Score 101.2; DB 4; Length 476;  
 Best Local Similarity 73.0%; Pred. No. 2,4e-20;  
 Matches 162; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

QY 1 GGAGAAATGTAAGTCTGGGCTCCCTG-----CAATCCGGTCCGATGTGGA 51  
 DB 208 GGAGAAATGTAAGTCTGGGCTCCCTGAAATTTGCAATGAGTGGCATGTGCA 267  
 QY 52 ACCTGTAAGTGAAGCCAGGCGCAGTGTGCAAGAGACTGTGTGTGACCAAGTCAGA 111  
 DB 268 ACGTGTAACTGAAATCAGGGTCAAGTGTGACATGAGACTGTGTGTGAGCAATGCATA 327  
 QY 112 TTTTGAAGAGAAATATGCGCGATGGCAAGGGTGA---TGACATGATGATTAC 168  
 DB 328 TTTAGCAATCAGAAACAGAAATGCGGCGCATCAATGATGATGATGACCCGCTGAAAC 387  
 QY 169 TGCAATGCAATATCTGCTGCTGTCCAGAAATCCCTTCAT 210  
 DB 388 TGCACTGGCCATCTCTGAGTGTCTGAGATGATCTTCAT 429

RESULT 4 444 bp mRNA linear EST 01-MAY-2002  
 BM401444  
 LOCUS JH2B04F Snake Bothrops insularis library IJ3 Bothrops insularis  
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401444 GI:20376072  
 VERSION BM401444.1 GI:20376072  
 KEYWORDS EST.  
 SOURCE Bothrops insularis (Island Jararaca)  
 ORGANISM Bothrops insularis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 444)  
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
 A survey of gene expression and diversity in the venom glands of  
 the pitviper snake Bothrops insularis through the generation of  
 expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE 22347338  
 PUBMED 12459276  
 COMMENT Contact: Paulo Lee Ho  
 Centro de Biotecnologia  
 Instituto Butantan  
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
 Tel: 55 11 37 26 7222 ext. 2083  
 Fax: 55 11 37 26 1505  
 Email: hoplee@usp.br

FEATURES  
 source This EST corresponds to cluster BTM30A (see Reference)  
 Seg primer: M13F.

Location/Qualifiers  
 1..444  
 /organism="Bothrops insularis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8723"  
 /tissue\_type="venom glands"  
 /clone\_lib="Snake Bothrops insularis library IJ3"  
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco  
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis  
 venom glands were primed with oligo-(dT) and reverse  
 transcribed to cDNA using Superscript Plasmid System for  
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
 were selected by size (350-600 pb and up 600 pb) in  
 agarose gel electrophoresis, linked to Eco RI adapters and  
 directionally cloned in pGEM11zf+ vector (Promega). ESTs  
 were generated from random clones and grouped in unique  
 sequences. The putative identification of each EST or  
 cluster was obtained through Blast searches (e-value <  
 e-05)."

ORIGIN

Query Match 47.1%; Score 100.4; DB 4; Length 444;  
 Best Local Similarity 75.8%; Pred. No. 4.2e-20;  
 Matches 138; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 31 AATCGTCTCGATGATGTCGAACCTGTAAGTGAAGCAGGCGCAGTGTGCAAGAGA 90  
 DB 30 AATCGTCTCGATGATGTCGAACCTGTAAGTGAAGCAGTGTGCAAGAGA 89  
 QY 91 CTGTGTGTGACCAAGTCAATTTATGAAAGAGAAATATCCCGATGGCAAGGGCT 150  
 DB 90 GAGTGTGTGACCAAGTCAATTTAAGGAGACAGATCAAGATCCGCTGCAAGAGAT 149  
 QY 151 GA---TGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207  
 DB 150 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 209  
 QY 208 CA 209  
 DB 210 CA 211

RESULT 5 357 bp mRNA linear EST 01-MAY-2002  
 BM401492  
 LOCUS JH2B04F Snake Bothrops insularis library IJ3 Bothrops insularis  
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401492 GI:20376120  
 VERSION BM401492.1 GI:20376120  
 KEYWORDS EST.  
 SOURCE Bothrops insularis (Island Jararaca)  
 ORGANISM Bothrops insularis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 357)  
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
 A survey of gene expression and diversity in the venom glands of  
 the pitviper snake Bothrops insularis through the generation of  
 expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE 22347338  
 PUBMED 12459276  
 COMMENT Contact: Paulo Lee Ho  
 Centro de Biotecnologia  
 Instituto Butantan  
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
 Tel: 55 11 37 26 7222 ext. 2083  
 Fax: 55 11 37 26 1505  
 Email: hoplee@usp.br

FEATURES  
 source This EST corresponds to cluster BTM11A (see Reference)  
 Seg primer: M13F.

Location/Qualifiers  
 1..357  
 /organism="Bothrops insularis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8723"  
 /tissue\_type="venom glands"  
 /clone\_lib="Snake Bothrops insularis library IJ3"  
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco  
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis  
 venom glands were primed with oligo-(dT) and reverse  
 transcribed to cDNA using Superscript Plasmid System for  
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
 were selected by size (350-600 pb and up 600 pb) in  
 agarose gel electrophoresis, linked to Eco RI adapters and  
 directionally cloned in pGEM11zf+ vector (Promega). ESTs  
 were generated from random clones and grouped in unique  
 sequences. The putative identification of each EST or  
 cluster was obtained through Blast searches (e-value <  
 e-05)."

ORIGIN

Query Match 47.0%; Score 100.2; DB 4; Length 357;  
 Best Local Similarity 72.9%; Pred. No. 4.6e-20;  
 Matches 161; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

1 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTGCA 51  
 |||||  
 56 GGAGAGAAATGATGACTGTGGCGCTCTGCAAAATTGTGCAATCCGCTGTGATGCTGCA 115  
 |||||  
 52 ACCTGTAACTGAGACCAAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGCA 111  
 |||||  
 116 ACCTGTAACTGAGACCAAGTGTGAGTGTGATGTGAGAGTGTGACCACTGCA 175  
 |||||  
 112 TTATGAAGAAGAGACCAATATGCCGATGGCAGAGGTGA---TGACATGATGATTAC 168  
 |||||  
 176 TTTAAAGACCAAGCATCAGAAATGCCGACAGAGAGTGTGACATTTCTGAAGC 235  
 |||||  
 169 TGCATGGCAATCTGCTGTGCTGCCAGAAATCCCTTCCA 209  
 |||||  
 236 TGCATGGCAATCTGCTGTGAGTGTCCATAGTACTTCCA 276  
 |||||

RESULT 6  
 BM401556 432 bp mRNA linear EST 01-MAY-2002  
 LOCUS JH3F08F Snake Bothrops insularis library IJ3 Bothrops insularis  
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.  
 ACCESSION BM401556  
 VERSION BM401556.1 GI:20376184  
 KEYWORDS EST.  
 SOURCE Bothrops insularis (Island Jararaca)  
 ORGANISM Bothrops insularis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroides;  
 Viperidae; Crotalinae; Bothrops.  
 1 (bases 1 to 432)  
 Juncqueira-de-Azevedo, I.L.M. and Ho, P.L.  
 A survey of gene expression and diversity in the venom glands of  
 the pitviper snake Bothrops insularis through the generation of  
 expressed sequence tags (ESTs)  
 JOURNAL Gene 299 (1-2), 279-291 (2002)  
 MEDLINE 22347338  
 PUBMED 12459276  
 COMMENT Contact: Paulo Lee Ho  
 Centro de Biotecnologia  
 Instituto Butantan  
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
 Tel: 55 11 37 26 7222 ext. 2083  
 Fax: 55 11 37 26 1505  
 Email: hoplee@usp.br  
 This EST corresponds to cluster BTM11A (see Reference)  
 Seq primer: M13F.  
 Location/Qualifiers  
 source  
 1..432  
 /organism="Bothrops insularis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8723"  
 /feature\_type="venom glands"  
 /clone\_lib="Snake Bothrops insularis library IJ3"  
 /note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco  
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis  
 venom glands were primed with oligo-(dT) and reverse  
 transcribed to cDNA using Superscript Plasmid System for  
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
 were selected by size (350-600 pb and up 600 pb) in  
 agarose gel electrophoresis, linked to Eco RI adapters and  
 directionally cloned in pGEM11zf+ vector (Promega). ESTs  
 were generated from random clones and grouped in unique  
 sequences. The putative identification of each EST or  
 cluster was obtained through Blast searches (e-value <  
 e-05)."

## ORIGIN

Query Match

47.0%; Score 100.2; DB 4; Length 432;

Best Local Similarity 72.9%; Pred. No. 4.8e-20;  
 Matches 161; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

1 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTGCA 51  
 |||||  
 162 GGAGAGAAATGATGACTGTGGCGCTCTGCAAAATTGTGCAATCCGCTGTGATGCTGCA 241  
 |||||  
 52 ACCTGTAACTGAGACCAAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGCA 111  
 |||||  
 242 ACCTGTAACTGAGACCAAGTGTGAGTGTGATGTGAGAGTGTGACCACTGCA 301  
 |||||  
 112 TTATGAAGAAGAGACCAATATGCCGATGGCAGAGGTGA---TGACATGATGATTAC 168  
 |||||  
 302 TTTAAAGACCAAGCATCAGAAATGCCGACAGAGAGTGTGACATTTCTGAAGC 361  
 |||||  
 169 TGCATGGCAATCTGCTGTGCTGCCAGAAATCCCTTCCA 209  
 |||||  
 362 TGCATGGCAATCTGCTGTGAGTGTCCATAGTACTTCCA 402  
 |||||

RESULT 7  
 BM401456 377 bp mRNA linear EST 01-MAY-2002  
 LOCUS JH1C08F Snake Bothrops insularis library IJ3 Bothrops insularis  
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.  
 ACCESSION BM401456  
 VERSION BM401456.1 GI:20376084  
 KEYWORDS EST.  
 SOURCE Bothrops insularis (Island Jararaca)  
 ORGANISM Bothrops insularis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroides;  
 Viperidae; Crotalinae; Bothrops.  
 1 (bases 1 to 377)  
 Juncqueira-de-Azevedo, I.L.M. and Ho, P.L.  
 A survey of gene expression and diversity in the venom glands of  
 the pitviper snake Bothrops insularis through the generation of  
 expressed sequence tags (ESTs)  
 JOURNAL Gene 299 (1-2), 279-291 (2002)  
 MEDLINE 22347338  
 PUBMED 12459276  
 COMMENT Contact: Paulo Lee Ho  
 Centro de Biotecnologia  
 Instituto Butantan  
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
 Tel: 55 11 37 26 7222 ext. 2083  
 Fax: 55 11 37 26 1505  
 Email: hoplee@usp.br  
 This EST corresponds to cluster BTM06A (see Reference)  
 Seq primer: M13F.  
 Location/Qualifiers  
 source  
 1..377  
 /organism="Bothrops insularis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8723"  
 /feature\_type="venom glands"  
 /clone\_lib="Snake Bothrops insularis library IJ3"  
 /note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco  
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis  
 venom glands were primed with oligo-(dT) and reverse  
 transcribed to cDNA using Superscript Plasmid System for  
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
 were selected by size (350-600 pb and up 600 pb) in  
 agarose gel electrophoresis, linked to Eco RI adapters and  
 directionally cloned in pGEM11zf+ vector (Promega). ESTs  
 were generated from random clones and grouped in unique  
 sequences. The putative identification of each EST or  
 cluster was obtained through Blast searches (e-value <  
 e-05)."

## ORIGIN

Query Match

46.1%; Score 98.2; DB 4; Length 377;

Matches 159; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

QY 4 GAAGAACTGCTGCTGGGCTCTCTG-----CAATCCGTCGTCGATGTCGAC 54  
Db 1 GAGAAATGCTACTGTGGCATCTCTGAAATTTGTCAAAATGATGCTGCTGACAG 60  
QY 55 TGTAACTGAGACCAAGGGGCGGCACTGTGTCAGAAAGCACTGTGTTGTGACCAATGATTT 114  
Db 61 TGTAACTGAAATCAGGGTCACTGTGTCAGATGAAAGCACTGTGTTGTGACCAATGATTT 120  
QY 115 ATGAAGAGAGAAATATGCGCGGATGCAAGGGGCTA---TGACATGATGATTTACTGC 171  
Db 121 AGCAATATGAGAAAGAAATGCGGGCATCAATGATGATGATGACCCGGCTGAACACTGC 180  
QY 172 AATGCAATCTGCTGCTGCTGTCCAGAAATCCCTTCAT 210  
Db 181 ACTGGCAATCCTCTGAGTGTCTGACATGCTTCAT 219

RESULT 8 420 bp mRNA linear EST 01-MAY-2002  
LOCUS BM401655  
DEFINITION J12E03F Snake Bothrops insularis library IL3 Bothrops insularis  
CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401655  
VERSION BM401655.1 GI:20376283  
KEYWORDS EST.  
SOURCE Bothrops insularis (Island Jararaca)  
ORGANISM Bothrops insularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 420)  
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
TITLE A survey of gene expression and diversity in the venom glands of  
the pitviper snake Bothrops insularis through the generation of  
expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)  
MEDLINE 22347338  
PubMed 12459276  
COMMENT Contact: Paulo Lee Ho  
Centro de Biotecnologia  
Instituto Butantan  
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hoplee@usp.br  
This EST corresponds to cluster BTM16A (see Reference)  
Seq primer: M13F.

FEATURES  
source Location/Qualifiers  
1..420  
/organism="Bothrops insularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8723"  
/issue\_type="venom glands"  
/clone\_lib="Snake Bothrops insularis library IL3"  
/note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco  
RI; Site 2: Not I; 5' of mRNA from Bothrops insularis  
venom glands were primed with oligo-(dT) and reverse  
transcribed to cDNA using Superscript Plasmid System for  
cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
were selected by size (350-600 pb and up 600 pb) in  
agarose gel electrophoresis, linked to Eco RI adaptors and  
directionally cloned in pGEM11zf+ vector (Promega). ESTs  
were generated from random clones and grouped in unique  
sequences. The putative identification of each EST or  
cluster was obtained through Blast searches (e-value <  
e-05)."

## ORIGIN

Query Match 35.0%; Score 74.6; DB 4; Length 420;  
Best Local Similarity 74.5%; Pred. No. 4.3e-12;  
Matches 108; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 68 CAGGGCGCAGTGTGTCAGAAAGACTGTGTTGTGACCAATGATTTATGAAGAAGAA 127  
Db 5 CATGGGTAGAGTGAATCTGGAGAGTGTGTCAGACGACAGATTTAAGGAGCAGAA 64  
QY 128 CATATGCCCGATGTCAGAGGGGTGA---TGACATGATGATTAATGCAATGATCTG 184  
Db 65 CAGATGCCCGGACACCAAGAGTGTGATGATGATGATGATGATGATGATGATGATG 124  
QY 185 CTGGCTGTCCAGAAATCCCTTCCA 209  
Db 125 CTGACTGTCCACAGATGACTTCAA 149

RESULT 9 411 bp mRNA linear EST 01-MAY-2002  
LOCUS BM401433  
DEFINITION GH089F Snake Bothrops insularis library IL2 Bothrops insularis CDNA  
5' similar to Snake venom metalloproteinase, mRNA sequence.  
ACCESSION BM401433  
VERSION BM401433.1 GI:20376061  
KEYWORDS EST.  
SOURCE Bothrops insularis (Island Jararaca)  
ORGANISM Bothrops insularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 411)  
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.  
TITLE A survey of gene expression and diversity in the venom glands of  
the pitviper snake Bothrops insularis through the generation of  
expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)  
MEDLINE 22347338  
PubMed 12459276  
COMMENT Contact: Paulo Lee Ho  
Centro de Biotecnologia  
Instituto Butantan  
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900  
Tel: 55 11 37 26 7222 ext. 2083  
Fax: 55 11 37 26 1505  
Email: hoplee@usp.br  
This EST corresponds to cluster BTM06A (see Reference)  
Seq primer: M13F.

FEATURES  
source Location/Qualifiers  
1..411  
/organism="Bothrops insularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8723"  
/issue\_type="venom glands"  
/clone\_lib="Snake Bothrops insularis library IL2"  
/note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco  
RI; Site 2: Not I; 5' of mRNA from Bothrops insularis  
venom glands were primed with oligo-(dT) and reverse  
transcribed to cDNA using Superscript Plasmid System for  
cDNA Synthesis and Cloning (Life Technologies). The cDNAs  
were selected by size (350-600 pb and up 600 pb) in  
agarose gel electrophoresis, linked to Eco RI adaptors and  
directionally cloned in pGEM11zf+ vector (Promega). ESTs  
were generated from random clones and grouped in unique  
sequences. The putative identification of each EST or  
cluster was obtained through Blast searches (e-value <  
e-05)."

## ORIGIN

Query Match 32.0%; Score 68.2; DB 4; Length 411;  
Best Local Similarity 69.9%; Pred. No. 4.2e-10;  
Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 61 CTGAGACCAAGGGCGGAGTGTGTCAGAAAGACTGTGTTGTGACCAATGATTTATGAAA 120  
Db 1 CTGAATTCAGGGTCAAGTGTGACATGAGACTGTGTTGTGACCAATGATTTATGAAA 60

```

Qy 121 GAGAGACAAATATGCGGATGCGAGGGGTGA---TGACATGATGATTACTGCATATGC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCAGGACAGATGCGCGGATCATGATGATGATGACCGGCTGAACAATGCACATGCGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 178 ATATCTGCTGCTGTCCAGAAATCCCTTCAT 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CAATCCTCTGAGTGTCTGACAGATGTCTTCAT 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
BM401391 474 bp mRNA linear EST 01-MAY-2002
LOCUS GH010F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
DEFINITION 5' similar to Snake venom metalloproteinase, mRNA sequence.
ACCESSION BM401391
VERSION BM401391.1 GI:20376019
KEYWORDS EST
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE 1 (bases 1 to 474)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITM06A (see Reference)
Seq primer: M13F.
Location/Qualifiers
source 1..474
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/clone_lib="Snake Bothrops insularis library IL2"
/issue_type="Venom glands"
/notes="Organ: Venom glands; Vector: pGEM11zf+; Site_1: Eco
RI; Site_2: Not I; 5ug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

## ORIGIN

```

Query Match 32.0%; Score 68.2; DB 4; Length 474;
Best Local Similarity 69.9%; Pred. No. 4.3e-10;
Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
```

```

Qy 61 CTGAGACCAAGGGCCAGTGTGCAAGAGACTGTGTGTGACCGATGATTATGAAA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CTGAATACAGGGTCACTGTGACATGACATGACATGTCATCAATTTAGGAAA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 GAGGACAAATATGCGCGATGCGAAGGGGTGA---TGACATGATGATTACTGCATGCG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCAGGACAGATGCGCGGATCATGATGATGATGACCGGCTGAACAATGCACATGCGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 178 ATATCTGCTGCTGTCCAGAAATCCCTTCAT 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

Db 121 CAATCCTCTGAGTGTCTGACAGATGTCTTCAT 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

RESULT 11
BM401397 527 bp mRNA linear EST 01-MAY-2002
LOCUS GH020F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
DEFINITION 5' similar to Snake venom metalloproteinase, mRNA sequence.
ACCESSION BM401397
VERSION BM401397.1 GI:20376025
KEYWORDS EST
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE 1 (bases 1 to 527)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITM06A (see Reference)
Seq primer: M13F.
Location/Qualifiers
source 1..527
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/clone_lib="Snake Bothrops insularis library IL2"
/issue_type="Venom glands"
/notes="Organ: Venom glands; Vector: pGEM11zf+; Site_1: Eco
RI; Site_2: Not I; 5ug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

## ORIGIN

```

Query Match 32.0%; Score 68.2; DB 4; Length 527;
Best Local Similarity 69.9%; Pred. No. 4.5e-10;
Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
```

```

Qy 61 CTGAGACCAAGGGCCAGTGTGCAAGAGACTGTGTGTGACCGATGATTATGAAA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CTGAATACAGGGTCACTGTGACATGACATGTCATCAATTTAGGAAA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 GAGGACAAATATGCGCGATGCGAAGGGGTGA---TGACATGATGATTACTGCATGCG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCAGGACAGATGCGCGGATCATGATGATGATGACCGGCTGAACAATGCACATGCGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 178 ATATCTGCTGCTGTCCAGAAATCCCTTCAT 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CAATCCTCTGAGTGTCTGACAGATGTCTTCAT 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 12



```

VERSION      BM401393.1  GI:20376021
KEYWORDS     EST.
SOURCE       Bothrops insularis (Island Jararaca)
ORGANISM     Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodactyla; Squamata; Sclerozoa; Serpentes; Cnidaria;
Viperidae; Crotalinae; Bothrops.
REFERENCE    1 (bases 1 to 565)
AUTHORS      Junqueira-de-Azevedo, I.L.M. and Ho, P.D.
TITLE        A survey of gene expression and diversity in the venom glands of
             the pitviper snake Bothrops insularis through the generation of
             expressed sequence tags (ESTs)
JOURNAL      Gene 299 (1-2), 279-291 (2002)
MEDLINE      22347338
COMMENT      12459276
             Location: Paulo Lee Ho
             Centro de Biotecnologia
             Instituto Butantan
             Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
             Tel: 55 11 37 26 7232 ext. 2083
             Fax: 55 11 37 26 1505
             Email: hopleeusp.br
             This EST corresponds to cluster BTW064 (see Reference)
             Seq primer: M3F.
FEATURES
    source
        location/Qualifiers
            1..565
            /organism="Bothrops insularis"
            /mol_type="mRNA"
            /db_xref="taxon:8723"
            /tissue_type="venom glands"
            /clone_lib="Snake Bothrops insularis library IL2"
            /note="Organ: Venom glands; Vector: pGSM1zf+; Site_1: Eco
            RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
            venom glands were primed with oligo- (dT) and reverse
            transcribed to cDNA using Superscript Plasmid System for
            cDNA Synthesis and Cloning (Life Technologies). The cDNAs
            were selected by size (350-600 pb and up 600 pb) in
            agarose gel electrophoresis, linked to Eco RI adapters and
            directionally cloned in pGSM1zf+ vector (Promega). ESTs
            were generated from random clones and grouped in unique
            sequences. The putative identification of each EST or
            cluster was obtained through Blast searches (e-value <
            e-05)."
ORIGIN
Query Match      32.0%; Score 68.2; DB 4; Length 565;
Best Local Similarity 69.9%; Pred. No. 4.5e-10;
Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Sillurans  
1 (bases 1 to 845)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.

FEATURES	Location/Qualifiers
source	1. .845

/note=Vector: pExprpress-1; Site\_1: EcoRV; Site\_2: NotI; Bulk tissue was collected from a whole 10 month old male from the P6 strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExprpress-1. Library was size-selected for >1.5 kb fragments for an average insert size of 1.92 kb. Library was normalized to Cots with a 180-fold reduction of actin. A non-normalized version of this library is also available (NICHD XGC Sw1). Library was constructed by Open Biosystems (Huntsville, AL). PLEASE NOTE: This library contains high level of contamination by tubifex"

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 863) Huang,G.M., Ng,W.L., Farakas,J., He,L., Liang,H.A., Gordon,D., Yu,J and Hood,L. Prostate cancer expression profiling by cDNA sequencing analysis
JOURNAL	Genomics 55 (2), 178-186 (1999)
MEDLINE	99339982
PUBMED	10409425
COMMENT	Contact: Guyang Matthew Huang

FEATURES	Location/Qualifiers
source	1. .863

## ORIGIN

Query Match	28.5%	Score 60.6	DB 1	Length 863
Best Local Similarity	59.7%	Pred. No. 1.2e-07		
Matches 120	Conservative	0	Mismatches 79	Indels 2
			Gaps	1
Qy	7	GAATGTACTGTGGGGGCTCCCTGCAAAATCCGTGCTGGAGTCTGCACACCTGTAACTGACA	66	
Db	236	GAACAGAGATGTGGCCCTTATTGGGAAACAATGCTGTGATATTTGCCACATGTGATTTAAA	295	
Qy	67	CCAGGGGCGCATGTGTGCAGAGACACTGTGTTGTACACAGTCAGATTATGAAGAAGGA	126	
Db	296	GCGGGTTAAACTGTGTGTGAAGAGACATGCTGGGAAAACGTCTATTATGTCAAAAGA	355	
Qy	127	ACAAATATGCCGATGGCAAGGGGTGAT--GACATGATGATTATCTGCAAATGGCATACTG	184	
Db	356	ACAAATGTGTAGGCCCTTCCTTTGAAGAAATGACACTCCCTGAATATTTGCAATGGGTACTCG	415	
Qy	185	CTGAGCTGTCCAGAAATCCCT	205	
Db	416	CATCATGCCCAAAAACCACT	436	

Search completed: December 3, 2004, 20:08:33  
Job time : 2977 secs

RESULT 15				
A1525705	A1525705	863 bp	mRNA	linear EST 09-AUG-1998
LOCUS				
DEFINITION	PT13.04_H03.r tumor1 Homo sapiens CDNA 5'			mRNA sequence.
ACCESSION	A1525705			
VERSION	A1525705.1 GI:4439840			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 21:14:23 ; Search time 51 Seconds

(without alignments)  
137.722 Million cell updates/sec

Title: US-10-089-473a-1

Perfect score: 433  
Sequence: 1 EAGEBCDCGAPANPCDDAAT.....DMDDYNGISAGCPRNPFHA 73

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_79:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	94.5	73	2	A59410 platelet aggregati
2	400	92.4	71	2	A59409 platelet-aggregati
3	400	92.4	71	2	A59411 platelet-aggregati
4	392.5	90.6	71	2	A33990 applaagin - easter
5	391	90.3	73	2	A23731 albolabrin - green
6	391	90.3	73	2	E35982 trigramin gamma -
7	386	89.1	480	1	A10065 trigramin precursor
8	383.5	88.6	484	1	UC8020 metalloproteinase
9	379	87.5	73	2	D59882 trigramin beta-2 -
10	356	82.2	72	2	B33020 platelet aggregati
11	355	82.0	72	2	E43019 platelet aggregati
12	350	82.0	73	2	E43019 platelet aggregati
13	348	80.4	71	2	G43019 platelet aggregati
14	347	80.1	73	2	B40003 platelet aggregati
15	344	79.4	73	2	A43020 platelet aggregati
16	344	79.4	73	2	H43019 platelet aggregati
17	343	79.2	72	2	F43019 platelet aggregati
18	343	79.2	73	2	C43019 platelet aggregati
19	341	78.8	73	2	A43019 platelet aggregati
20	339	78.3	71	2	A59412 KGD-bearing plate
21	339	78.3	73	2	A40003 platelet aggregati
22	335	77.4	72	2	B43019 platelet aggregati
23	335	77.4	72	2	D43019 platelet aggregati
24	335	77.4	72	2	S43125 trilmucin precursor
25	331	76.9	71	2	A59413 platelet-aggregat
26	331	76.4	71	2	S3168 fibrinolytic prote
27	325	75.1	481	2	UC4342 fibrinolytic prote
28	316	73.0	70	2	A58649 hemorhagic protei
29	304	70.2	478	2	UC1301 hemorhagic protei

30	293	67.7	478	2	A43296 atrolysin E (EC 3.
31	281	64.9	75	2	UX0169 cytoolic factor I
32	277.5	64.1	83	2	F35982 bitan alpha - puff
33	273	63.0	616	2	A55796 ecarin precursor -
34	269.5	62.2	83	2	A34156 bitistatin - puff
35	256	59.1	610	2	UC7530 vascular apoptosis
36	254	58.7	429	2	A42972 coagulation factor
37	251	58.0	610	2	JC6056 halyase - Gloydiu
38	237	54.7	571	2	S24789 jararagin C, precu
39	237	54.7	609	2	S55270 catrocollastatin p
40	234	54.0	209	2	UX0266 platelet aggregati
41	224	54.0	419	2	A59414 metalloproteinase
42	232	53.6	419	2	S41607 atrolysin A (EC 3.
43	232	53.6	478	2	JC4880 fibrinolytic metal
44	231	53.3	416	2	A37877 hemorhagic protei
45	228.5	52.8	735	2	G02937 fertillin beta - cr

#### ALIGNMENTS

##### RESULT 1

A59410 platelet aggregation disintegrin (brevicaudin) 1b, venom - Gloydius haly's brevicaudus

C/Species: Gloydius haly's brevicaudus

C/Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004

C/Accession: A59410

R/terada, S.

Fukuoka Univ. Sci. Reports 30, 71-78, 2000

A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd

A/Reference number: A59409

A/Accession: A59410

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-73 <TER>

A/Cross-references: UNIPROT:Q90220

C/Keywords: anticoagulant, integrin inhibitor, venom

Query Match 94.5%; Score 409; DB 2; Length 73;

Best Local Similarity 91.8%; Pred. No. 3.3e-32;

Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY	1	EAGEBCDCGAPANPCDDAATCKLRGACAEGLCCDGRFMKEGTCIMARSDMDVDCN	60
DB	1	EAGEBCDCGSPNPPCDATCKLRGACAEGLCCDGRFMKGTVCRIARSDMDVDCN	60
QY	61	GISAGCPRNPFHA 73	
DB	61	GISAGCPRNPFHA 73	

##### RESULT 2

A59409 platelet-aggregation disintegrin (brevicaudin) 2b, venom - Gloydius haly's brevicaudus

C/Species: Gloydius haly's brevicaudus

C/Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004

C/Accession: A59409

R/terada, S.

Fukuoka Univ. Sci. Reports 30, 71-78, 2000

A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd

A/Reference number: A59409

A/Accession: A59409

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-71 <TR>

A/Cross-references: UNIPROT:Q90WC0

C/Keywords: anticoagulant, integrin inhibitor, venom

Query Match 92.4%; Score 400; DB 2; Length 71;  
Best Local Similarity 93.0%; Pred. No. 2.3e-31;  
Matches 66; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GEEBCDCGAPANPCDDAATCKLRGACAEGLCCDGRFMKEGTCIMARSDMDVDCN 62

Db 1 GEECCGSPNPPCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60  
QY 63 SAGCPRNPFA 73  
Db 61 SAGCPRNPFA 71

## RESULT 3

A59411  
platelet-aggregation disintegrin (previcaudin) 1a - Gloydus halys brevicaudus  
C/Species: Gloydus halys brevicaudus  
C/Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004  
C/Accession: A59411  
R/Retard, S.  
Fukuoka Univ. Sci. Reports 30, 71-78, 2000  
A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd  
A/Reference number: A59409  
A/Accession: A59411  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-71 <TER>  
A/Cross-references: UNIPROT:Q90220  
C/Keywords: antiscagulant; integrin inhibitor; venom

Query Match 92.4%; Score 400; DB 2; Length 71;  
Best Local Similarity 91.5%; Pred. No. 2.3e-31;  
Matches 65; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GEECCGAPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 62  
Db 1 GEECCGSPNPPCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
QY 63 SAGCPRNPFA 73  
Db 61 SAGCPRNPFA 71

## RESULT 4

A33990  
aplaggin - eastern cottonmouth  
C/Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)  
C/Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004  
C/Accession: A33990  
R/Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chcw, E.P.; Marzoc, U.M.; Harper, L.A.; Mara  
Proc. Natl. Acad. Sci. U.S.A. 86, 8050-8054, 1989  
A/Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inhi  
A/Reference number: A33990; MUID:90046735; PMID:2510158  
A/Accession: A33990  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-71 <CHA>  
A/Cross-references: UNIPROT:P16338  
C/Suprafamily: unassigned disintegrins; disintegrin homology  
F.1-68/Domain: disintegrin homology (fragment) <DIS>

Query Match 90.6%; Score 392.5; DB 2; Length 71;  
Best Local Similarity 90.3%; Pred. No. 1.2e-30;  
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
Db 1 EAGEECDCGSPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 59  
QY 61 GISAGCPRNPFA 72  
Db 60 GISAGCPRNPFA 71

## RESULT 5

A23731  
albolabrin - green pit viper  
C/Species: Trimereurus albolabris (green pit viper)

C/Date: 28-Feb-1992 #sequence\_revision 23-Aug-1997 #text\_change 09-Jul-2004  
C/Accession: A23731; S43021  
R/Calvete, J.J.; Schaefer, W.; Soszka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarow  
Biochemistry 30, 5225-5229, 1991  
A/Title: Identification of the disulfide bond pattern in albolabrin, an RGD-containing  
itory activity.  
A/Reference number: A23731; MUID:91242430; PMID:2036389

A/Accession: A23731  
A/Molecule type: protein  
A/Residues: 1-73 <CAL>  
A/Cross-references: UNIPROT:P17496  
R/Jaseja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.L.  
Bull. J. Biochem 218, 853-860, 1993  
A/Title: (1)H-NMR studies and secondary structure of the RGD-containing snake toxin, al  
A/Reference number: S43021; MUID:94105384; PMID:8281937  
A/Accession: S43021  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-73 <JAS>

C/Function: inhibits cell adhesion and platelet aggregation  
A/Description: unassigned disintegrins; disintegrin homology  
C/Suprafamily: venom  
C/Keywords: Venom  
F.1-68/Domain: disintegrin homology (fragment) <DIS>  
F.1-53/Region: cell attachment (R-G-D) motif  
F.29-59,47-66/Disulfide bonds: #status experimental

Query Match 90.3%; Score 391; DB 2; Length 73;  
Best Local Similarity 87.7%; Pred. No. 1.6e-30;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
Db 1 EAGEECDCGSPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
QY 61 GISAGCPRNPFA 73  
Db 61 GISAGCPRNPFA 73

## RESULT 6

E35982  
trigemin gamma - Indian green tree viper  
C/Species: Trimereurus gramineus (Indian green tree viper)  
C/Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Aug-2004  
C/Accession: E35982  
R/Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Delisher, T.A.; B  
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990  
A/Title: Platelet glycoprotein IIb/IIIa protein antagonists from snake venoms: evidence  
A/Reference number: A35982; MUID:90207217; PMID:2320569  
A/Accession: E35982  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-73 <DEN>  
A/Cross-references: UNIPROT:P17496  
C/Suprafamily: disintegrin homology (fragment) <DIS>  
F.1-69/Domain: disintegrin homology (fragment) <DIS>  
F.51-53/Region: cell attachment (R-G-D) motif

Query Match 90.3%; Score 391; DB 2; Length 73;  
Best Local Similarity 87.7%; Pred. No. 1.6e-30;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
Db 1 EAGEECDCGSPNPPCCDAATCKLRPGACAEGLCCDQCFMKKGTICRRARAGDDMDYCN 60  
QY 61 GISAGCPRNPFA 73  
Db 61 GISAGCPRNPFA 73

## RESULT 7

A30065  
trigramin precursor - Indian green tree viper  
N/Contains: hemoregulatory proteinase (EC 3.4.24.-); platelet aggregation inhibitor (disint  
C/Species: Trimeresurus gramineus (Indian green tree viper)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C/Accession: J12589; A30065; A29784  
R/Neper, M.P.; Jacobson, M.A.  
Nucleic Acids Res. 19, 4255, 1990  
A/Title: Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin.  
A/Reference number: J12589; MUID:90332429; PMID:2377470  
A/Accession: J12589  
A/Molecule type: mRNA  
A/Residues: 1-480 <NEE>  
A/Cross-references: UNIPROT:P15503; EMBL:X51530; NID:964407; PIDN:CA35910.1; PID:964408  
A/Note: translation of the signal sequence and the mature protein but not of the propept  
R/Huang, T.F.; Holt, J.C.; Kizdy, E.F.; Niewiarowski, S.  
Biochemistry 28, 661-666, 1989  
A/Title: Trigramin: primary structure and its inhibition of von Willebrand factor bindin  
A/Reference number: A30065; MUID:89229063; PMID:2653425  
A/Accession: A30065  
A/Molecule type: protein  
A/Residues: 408-479 <HUA>  
R/Huang, T.F.; Holt, J.C.; Lukaeiwicz, H.; Niewiarowski, S.  
J. Biol. Chem. 262, 16157-16163, 1987  
A/Title: Trigramin, A low molecular weight peptide inhibiting fibrinogen interaction with  
A/Reference number: A29784; MUID:88058981; PMID:3680247  
A/Accession: A29784  
A/Molecule type: protein  
A/Residues: 408-419 <HUA>  
C/Superfamily: trigramin precursor, disintegrin homology  
C/Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc; zymo  
F/1-18/Domain: signal sequence #status predicted <SIG>  
F/398-476/Domain: disintegrin homology <DIS>  
F/408-479/Product: trigramin #status experimental <MAT>  
F/458-460/Region: cell attachment (R-G-D) motif  
F/427/Binding site: carbohydrate (asn) (covalent) #status predicted  
F/333,337,343/Binding site: zinc (His) #status predicted  
F/334/Active site: Glu #status predicted

Query Match 89.1%; Score 386; DB 1; Length 480;  
Best Local Similarity 84.9%; Pred. No. 1.9e-29;  
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 60  
DB 408 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 467

QY 61 GISAGCPRNPFA 73  
DB 468 GRSAGCPRNPFA 480

RESULT 8  
JC8020  
metalloproteinase-disintegrin protein, Jerdonitn - Trimeresurus jerdoni  
C/Species: Trimeresurus jerdoni  
C/Date: 04-Apr-2004 #sequence\_revision 04-Apr-2004 #text\_change 04-Apr-2004  
C/Accession: JC8020; PC7231  
R/Chen, R.Q.; Jin, Y.; Wu, J.B.; Zhou, X.D.; Lu, Q.M.; Wang, W.Y.; Xiong, Y.L.  
Biochem. Biophys. Res. Commun. 310, 182-187, 2003  
A/Title: A new protein structure of P-II class snake venom metalloproteinases: It compli  
A/Reference number: JC8020; PMID: 14511668  
A/Accession: JC8020  
A/Molecule type: mRNA  
A/Residues: 1-484 <CHE>  
A/Cross-references: GB:AY364231  
A/Experimental source: Crude venom  
A/Accession: PC7231  
A/Molecule type: protein  
A/Residues: 206-214;221-233;299-308;310-344;451-453;460-484 <CH2>  
A/Comment: This protein, a new metalloproteinase-disintegrin protein, belongs to the cla  
sion with IC50 of 120nM.  
C/Keywords: Jerdonitn; metalloproteinase-disintegrin; platelet aggregation; SWP

Query Match 88.6%; Score 383.5; DB 2; Length 484;  
Best Local Similarity 82.9%; Pred. No. 3.3e-29;  
Matches 63; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

QY 1 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 57  
DB 409 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 468

QY 58 YCNGISAGCPRNPFA 73  
DB 469 YCNGISAGCPRNPFA 484

RESULT 9  
D35982  
trigramin beta-2 - Indian green tree viper  
N/Contains: trigramin beta-1  
C/Species: Trimeresurus gramineus (Indian green tree viper)  
C/Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Aug-2004  
C/Accession: D35982; C35982  
R/Dennis, M.S.; Hentzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; B  
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990  
A/Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence  
A/Reference number: A35982; MUID:90207217; PMID:2320569  
A/Accession: D35982  
A/Molecule type: protein  
A/Residues: 1-73 <DEN>  
A/Cross-references: UNIPROT:P17495  
A/Accession: C35982  
A/Molecule type: protein  
A/Residues: 1-72 <DE2>  
C/Superfamily: disintegrin homology  
C/Keywords: Venom  
F/1-73/Product: trigramin beta-2 #status experimental <MA2>  
F/1-72/Product: trigramin beta-1 #status experimental <MA1>  
F/1-72/Domain: disintegrin homology (fragment) <DIS>  
F/51-53/Region: cell attachment (R-G-D) motif

Query Match 87.5%; Score 379; DB 2; Length 73;  
Best Local Similarity 84.9%; Pred. No. 2.3e-29;  
Matches 62; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 60  
DB 1 EAGEBCDCCGAPNPPCCDAATCKLRPGACAGLCCDQCFMKEGTICRMARDDMDYCN 60

QY 61 GISAGCPRNPFA 73  
DB 61 GRSAGCPRNPFA 73

RESULT 10  
B43020  
platelet aggregation disintegrin (cereberin), venom - Arizona black rattlesnake  
C/Species: Crotalus viridis cerberus (Arizona black rattlesnake)  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: B43020  
R/Schattorouh, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten,  
J. Biol. Chem. 268, 1058-1065, 1993  
A/Title: Characterization of the integrin specificities of disintegrins isolated from A  
A/Reference number: A43019; MUID:93123215; PMID:8419314  
A/Accession: B43020  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-72 <SCA>  
A/Cross-references: UNIPROT:P1985  
C/Superfamily: unassigned disintegrins; disintegrin homology  
F/3-69/Domain: disintegrin homology <DIS>

Query Match 82.2%; Score 356; DB 2; Length 72;  
Best Local Similarity 83.3%; Pred. No. 3.4e-27;  
Matches 60; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGSPANPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60  
QY 61 GISAGCPNPFH 72  
DB 61 QGADCPNPFH 72

## RESULT 11

143019  
platelet aggregation disintegrin (basillicin), venom - Mexican West-Coast rattlesnake  
C/Species: Crocalus basiliscus basiliscus (Mexican West-Coast rattlesnake)  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
C/Accession: 143019  
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arsten,  
J. Biol. Chem. 268, 1058-1065, 1993  
A/Title: Characterization of the integrin specificities of disintegrins isolated from Am  
A/Reference number: A43019; MUID:93123215; PMID:8419314  
A/Accession: 143019  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-72 <SCA>  
A/Cross-references: UNIPROT:P31981  
A/Superfamily: disintegrin homology  
F/3-68/Domain: disintegrin homology <DIS>

Query Match 82.0%; Score 355; DB 2; Length 72;  
Best Local Similarity 83.3%; Pred. No. 4.2e-27;  
Matches 60; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 61  
DB 1 AGEBCDGGSPANPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 62 ISAGCPNPFH 73  
DB 61 QGADCPNPFH 72

## RESULT 12

E43019  
platelet aggregation disintegrin (lachesin), venom - bushmaster  
C/Species: Lachesis muta (bushmaster)  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
C/Accession: E43019  
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arsten,  
J. Biol. Chem. 268, 1058-1065, 1993  
A/Title: Characterization of the integrin specificities of disintegrins isolated from Am  
A/Reference number: A43019; MUID:93123215; PMID:8419314  
A/Accession: E43019  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-73 <SCA>  
A/Cross-references: UNIPROT:P31990  
A/Superfamily: disintegrin homology  
F/3-69/Domain: disintegrin homology <DIS>

Query Match 80.8%; Score 350; DB 2; Length 73;  
Best Local Similarity 81.9%; Pred. No. 1.3e-26;  
Matches 59; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISAGCPNPFH 72  
DB 61 QGADCPNPFH 72

## RESULT 13

G43019  
platelet aggregation disintegrin (viridin), venom - prairie rattlesnake  
C/Species: Crotalus viridis viridis (prairie rattlesnake)  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
C/Accession: G43019  
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arsten,  
J. Biol. Chem. 268, 1058-1065, 1993  
A/Title: Characterization of the integrin specificities of disintegrins isolated from A  
A/Reference number: A43019; MUID:93123215; PMID:8419314  
A/Accession: G43019  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-71 <SCA>  
A/Cross-references: UNIPROT:P31987  
A/Superfamily: disintegrin homology  
F/2-68/Domain: disintegrin homology <DIS>

Query Match 80.4%; Score 348; DB 2; Length 71;  
Best Local Similarity 81.7%; Pred. No. 1.9e-26;  
Matches 58; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 61  
DB 1 AGEBCDGGSPANPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 62 ISAGCPNPFH 72  
DB 61 QGADCPNPFH 71

## RESULT 14

B40003  
platelet aggregation disintegrin (tergeminin), venom - western massasauga  
C/Species: Sistrurus catenatus tergeminus (western massasauga)  
C/Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: B40003  
R/Scarborough, R.M.; Rose, J.W.; Hsu, M.A.; Phillips, D.R.; Fried, V.A.; Campbell, A.M.,  
J. Biol. Chem. 266, 9359-9362, 1991  
A/Title: Barbourin, A GPIIb-IIIa-specific integrin antagonist from the venom of Sistrurus  
A/Reference number: A40003; MUID:91236695; PMID:2033037  
A/Accession: B40003  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-73 <SCA>  
A/Cross-references: UNIPROT:P22828  
A/Superfamily: unassigned disintegrins; disintegrin homology  
F/3-69/Domain: disintegrin homology <DIS>

Query Match 80.1%; Score 347; DB 2; Length 73;  
Best Local Similarity 84.1%; Pred. No. 2.4e-26;  
Matches 58; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGSPANPPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISAGCPNPFH 69  
DB 61 QGADCPNPFH 69

## RESULT 15

A43020  
platelet aggregation disintegrin (jararacin), venom - jararacusu  
C/Species: Bothrops jararacus (jararacusu)  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 10-Jul-1998  
C/Accession: A43020  
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arsten,  
J. Biol. Chem. 268, 1058-1065, 1993  
A/Title: Characterization of the integrin specificities of disintegrins isolated from A  
A/Reference number: A43019; MUID:93123215; PMID:8419314  
A/Accession: A43020  
A/Status: preliminary

Mon Dec 6 09:02:52 2004

us-10-089-473a-1.rpr

Page 5

A;Molecule type: protein

A;Residues: 1-73 &lt;SCA&gt;

C; Superfamily: unassigned disintegrins; disintegrin homology

F3-69/Domain: disintegrin homology <DIS>

Query Match	Score	DB 2	Length
79.48	344	73	

Best Local Similarity 80.8%; Pred. No. 4.6e-26;

Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Dy  
1 EAGEBCDCGAPNPCCDATTCTLRPGAGCAEGICCDQCFMKESTICNARAGDDMDYCN 60

Dd  
1 EAGEBCDCGTGNPCCDATCTLTPGAACAEGLCCDQCFFKAGKICRAARGNDPDRCF 60

1 EAGEECDCGT PGNPCC

QY 61 GISAGCPRNPFHA 73

Db 61 GQSA DCPNRFHA 73

Search completed: December 3, 2004, 21:39:13

Job time : 51 secs

**This Page Blank (uspio)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 21:26:53 ; Search time 53 Seconds  
(without alignments)  
91.344 Million cell updates/sec

Title: US-10-089-473A-1

Perfect score: 433 EAGEBCDCGAPNPPCDAT.....DMDYCNISAGCPNPFH 73

Sequence: 1

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	402	92.8	72 6 5182260-21	Patent No. 5182260
2	402	92.8	73 6 5182260-2	Patent No. 5182260
3	395	91.2	73 4 US-05-776-268A-1	Sequence 1, Appl1
4	392.5	90.6	71 1 US-07-965-674-10	Sequence 10, Appl1
5	392.5	90.6	71 4 US-09-460-295B-7	Sequence 7, Appl1
6	392.5	90.6	71 5 PCT-US93-09523-10	Sequence 10, Appl1
7	391	90.3	73 1 US-07-965-674-14	Sequence 14, Appl1
8	391	90.3	73 2 US-08-993-165-15	Sequence 15, Appl1
9	391	90.3	73 4 US-08-243-640-13	Sequence 13, Appl1
10	391	90.3	73 4 US-08-929-847-15	Sequence 15, Appl1
11	391	90.3	73 4 US-09-460-295B-9	Sequence 9, Appl1
12	391	90.3	73 4 US-09-813-484-15	Sequence 15, Appl1
13	391	90.3	73 5 PCT-US93-09523-14	Sequence 14, Appl1
14	390	90.1	99 1 US-07-623-611-5	Sequence 5, Appl1
15	390	90.1	99 1 US-07-623-611-8	Sequence 8, Appl1
16	390	90.1	99 5 PCT-US91-09108-5	Sequence 5, Appl1
17	390	90.1	99 5 PCT-US91-09108-8	Sequence 8, Appl1
18	390	90.1	106 1 US-07-623-611-4	Sequence 4, Appl1
19	390	90.1	106 1 US-07-623-611-7	Sequence 7, Appl1
20	390	90.1	106 5 PCT-US91-09108-4	Sequence 4, Appl1
21	390	90.1	106 5 PCT-US91-09108-7	Sequence 7, Appl1
22	387	89.4	98 1 US-07-623-611-6	Sequence 6, Appl1
23	387	89.4	98 1 US-07-623-611-9	Sequence 9, Appl1
24	387	89.4	98 5 PCT-US91-09108-6	Sequence 6, Appl1
25	387	89.4	98 5 PCT-US91-09108-9	Sequence 9, Appl1
26	386	89.1	73 4 US-09-540-448-15	Sequence 15, Appl1
27	386	89.1	552 4 US-09-460-295B-8	Sequence 8, Appl1

28	384.5	88.8	71 1 US-07-602-847C-24	Sequence 24, Appl1
29	384	88.7	72 1 US-07-623-611-1	Sequence 1, Appl1
30	384	88.7	72 5 PCT-US91-09108-1	Sequence 1, Appl1
31	384	88.7	96 1 US-07-623-611-2	Sequence 2, Appl1
32	384	88.7	96 1 US-07-623-611-3	Sequence 3, Appl1
33	384	88.7	96 5 PCT-US91-09108-2	Sequence 2, Appl1
34	384	88.7	96 5 PCT-US91-09108-3	Sequence 3, Appl1
35	382	88.2	72 1 US-07-602-847C-23	Sequence 23, Appl1
36	371.5	85.8	73 1 US-07-965-674-5	Sequence 5, Appl1
37	371.5	85.8	73 5 PCT-US93-09523-5	Sequence 5, Appl1
38	368	85.0	483 4 US-09-460-295B-2	Sequence 2, Appl1
39	350	80.8	73 6 518899-6	Patent No. 518899
40	348	80.4	71 6 518899-11	Patent No. 518899
41	347	80.1	73 6 518899-3	Patent No. 518899
42	344	79.4	73 6 518899-2	Patent No. 518899
43	341.5	78.9	71 6 518899-13	Patent No. 518899
44	341	78.8	72 6 518899-9	Patent No. 518899
45	341	78.8	73 6 518899-4	Patent No. 518899

## ALIGNMENTS

```

RESULT 1
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:21:
; LENGTH: 72
5182260-21

Query Match          92.8%; Score 402; DB 6; Length 72;
Best Local Similarity 90.3%; Pred. No. 1.6e-30;
Matches 65; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDCGAPNPPCDATCKLRGACCAEGLCCDCCRFMKEGTICRMARQDDMDYCN 60
DB 1 EAGEBCDCGSPNPPCDATCKLRGACCAEGLCCDCCRFMKEGTICRRARQDDMDYCN 60

QY 61 GISAGCPNPFH 72
DB 61 GISAGCPNPFH 72

RESULT 2
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:

```

LENGTH: 73  
5182260-2

Query Match 92.8%; Score 402; DB 6; Length 73;  
Best Local Similarity 90.3%; Pred. No. 1.6e-30;  
Matches 65; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 2 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 61

QY 61 GISACCPNPFH 72  
DB 62 GISACCPNPFH 73

RESULT 3  
US-09-776-268A-1  
; Sequence 1, Application US/09776268A  
; Patent No. 6537551  
; GENERAL INFORMATION:  
; APPLICANT: KIM, DOO-SIK  
; APPLICANT: CHUNG, KWANG HOE  
; APPLICANT: KANG, JIN-CHEOL  
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT  
; FILE REFERENCE: 0136/1F733-US1  
; CURRENT APPLICATION NUMBER: US/09/776,268A  
; PRIOR FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: US 09/335,088  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: KR 99-20579  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: KR 98-23778  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Agkistrodon halys brevicaudus  
US-09-776-268A-1

Query Match 91.2%; Score 395; DB 4; Length 73;  
Best Local Similarity 90.4%; Pred. No. 7.1e-30;  
Matches 66; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISACCPNPFH 73  
DB 61 GISACCPNPFH 73

RESULT 4  
US-07-965-674-10  
; Sequence 10, Application US/07965674  
; Patent No. 5380646  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Linda C.  
; TITLE OF INVENTION: Thrombus Detection Using  
; TITLE OF INVENTION: Radiolabelled Disintegrins  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESS: Wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,674  
FILING DATE: 19921019  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-173  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5380646e  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-965-674-10

Query Match 90.6%; Score 392.5; DB 1; Length 71;  
Best Local Similarity 90.3%; Pred. No. 1.2e-29;  
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 59

QY 61 GISACCPNPFH 72  
DB 60 GISACCPNPFH 71

RESULT 5  
US-09-460-295B-7  
; Sequence 7, Application US/09460295B  
; Patent No. 6710030  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
; TITLE OF INVENTION: CONTOURSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS  
; FILE REFERENCE: 1279-338C3/09801388  
; CURRENT APPLICATION NUMBER: US/09/460,295B  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: US 09/163,047  
; PRIOR FILING DATE: 1998-08-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Agkistrodon piscivorus  
US-09-460-295B-7

Query Match 90.6%; Score 392.5; DB 4; Length 71;  
Best Local Similarity 90.3%; Pred. No. 1.2e-29;  
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 59

QY 61 GISACCPNPFH 72  
DB 60 GISACCPNPFH 71

RESULT 6  
PCT-US93-09523-10  
Sequence 10, Application PC/US9309523  
GENERAL INFORMATION:  
APPLICANT: Temple University - Of The Commonwealth  
APPLICANT: System of Higher Education  
APPLICANT: Knight, Linda C. and  
APPLICANT: Maurer, Alan H.  
TITLE OF INVENTION: Thrombus Detection Using  
TITLE OF INVENTION: Radiolabelled Disintegrins  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The  
ADDRESSEE: Commonwealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 965,674  
FILING DATE: 19 October 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-173 PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8363  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-09523-10

Query Match 90.6%; Score 392.5; DB 5; Length 71;  
Best Local Similarity 90.3%; Pred. No. 1,2e-29;  
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDCGAPANPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 60  
DB 1 EAGEBCDCGSPENPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 59  
QY 61 GISAGCPRNPFH 72  
DB 60 GISAGCPRNPFH 71

RESULT 7  
US-07-965-674-14  
Sequence 14, Application US/07965674  
Patent No. 5380646  
GENERAL INFORMATION:  
APPLICANT: Knight, Linda C.  
TITLE OF INVENTION: Thrombus Detection Using  
TITLE OF INVENTION: Radiolabelled Disintegrins  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSEE: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,674  
FILING DATE: 19921019  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-173  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8363  
TELEFAX: (215) 568-5549  
TELEX: No. 5380646e  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-965-674-14

Query Match 90.3%; Score 391; DB 1; Length 73;  
Best Local Similarity 87.7%; Pred. No. 1,6e-29;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDCGAPANPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 60  
DB 1 EAGEBCDCGSPANPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 60  
QY 61 GISAGCPRNPFH 73  
DB 61 GISAGCPRNPFH 73

RESULT 8  
US-08-993-165-15  
Sequence 15, Application US/08993165A  
Patent No. 6123923  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C  
APPLICANT: Wu, Yungliu  
TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use  
FILE REFERENCE: UNGR1224  
CURRENT APPLICATION NUMBER: US/08/993,165A  
CURRENT FILING DATE: 1997-12-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 15  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence  
US-08-993-165-15

Query Match 90.3%; Score 391; DB 3; Length 73;  
Best Local Similarity 87.7%; Pred. No. 1,6e-29;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDCGAPANPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 60  
DB 1 EAGEBCDCGSPANPCDDATCKLRPGACGAGLCCDQCFMKKGTTCRMARDDMDYCN 60  
QY 61 GISAGCPRNPFH 73

Db 61 GISAGCPRNPLHA 73

RESULT 9

US-09-243-640-13

Sequence 13, Application US/09243640

Patent No. 6521211

GENERAL INFORMATION:

APPLICANT: Unger, Evan C

APPLICANT: Shen, Dekang

APPLICANT: Wu, Guanli

TITLE OF INVENTION: No. 6521211el Methods Of Imaging And Treatment With Targeted

FILE REFERENCE: DUP-0463

CURRENT APPLICATION NUMBER: US/09/243,640

PRIOR FILING DATE: 1999-02-03

PRIOR APPLICATION NUMBER: 08/660,032

PRIOR FILING DATE: 1996-06-06

PRIOR APPLICATION NUMBER: 08/640,464

PRIOR FILING DATE: 1996-05-01

PRIOR APPLICATION NUMBER: 08/497,684

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 09/218,660

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: 60/073,913

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 13

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence

US-09-243-640-13

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCDDQCFMKKGTICRRARGDDLDYCN 60

Qy 61 GISAGCPRNPLHA 73

Db 61 GISAGCPRNPLHA 73

RESULT 10

US-08-929-847-15

Sequence 15, Application US/08929847

Patent No. 6548047

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions

FILE REFERENCE: BMS0441

CURRENT APPLICATION NUMBER: US/08/929,847

PRIOR FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentln version 3.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Completely synthetic sequence

US-08-929-847-15

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCDDQCFMKKGTICRRARGDDLDYCN 60

Qy 61 GISAGCPRNPLHA 73

Db 61 GISAGCPRNPLHA 73

RESULT 11

US-09-460-295B-9

Sequence 9, Application US/09460295B

Patent No. 6710030

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

TITLE OF INVENTION: CONTRASTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS

FILE REFERENCE: 1279-338C3/09801388

CURRENT APPLICATION NUMBER: US/09/460,295B

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/163,047

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentln version 3.1

SEQ ID NO 9

LENGTH: 73

TYPE: PRT

ORGANISM: Trimeresurus albolabris

US-09-460-295B-9

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCDDQCFMKKGTICRRARGDDLDYCN 60

Qy 61 GISAGCPRNPLHA 73

Db 61 GISAGCPRNPLHA 73

RESULT 12

US-09-813-484-15

Sequence 15, Application US/09813484

Patent No. 6716412

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseo

FILE REFERENCE: UNGR1600

CURRENT APPLICATION NUMBER: US/09/813,484

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 08/929,847

PRIOR FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentln version 3.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Completely synthetic sequence

US-09-813-484-15

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGECDCCGSPANPCDDATCKLLPQAQCGEGLCDDCGCFMKKGTTCRRARGGDDLDYCN 60  
QY 61 GISAGCPRNPFHA 73  
Db 61 GISAGCPRNPFHA 73

RESULT 13  
PCT-US93-09523-14  
Sequence 14, Application PC/TUS9309523  
GENERAL INFORMATION:  
APPLICANT: Temple University - Of The Commonwealth  
APPLICANT: System of Higher Education  
APPLICANT: Knight, Linda C. and  
APPLICANT: Maurer, Alan H.  
TITLE OF INVENTION: Thrombus Detection Using  
TITLE OF INVENTION: Radiolabelled Disintegrins  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The  
ADDRESSEE: Commonwealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 965,674  
FILING DATE: 19 October 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-173 PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8363  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-09523-14

Query Match 90.3%; Score 391; DB 5; Length 73;  
Best Local Similarity 87.7%; Pred. No. 1.6e-29;  
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EAGECCDCCGAPANPCDDATCKLRPQAQCAAGLCCDQCFMKKEGTTCRRARGGDDMDYCN 60  
Db 1 EAGECCDCCGSPANPCDDATCKLLPQAQCGEGLCDDCGCFMKKGTTCRRARGGDDLDYCN 60  
QY 61 GISAGCPRNPFHA 73  
Db 61 GISAGCPRNPFHA 73

RESULT 14  
US-07-623-611-5  
Sequence 5, Application US/07623611  
Patent No. 5242810  
GENERAL INFORMATION:  
APPLICANT: Maraganore, John M.  
APPLICANT: Chao, Betty H.

APPLICANT: Strauch, Kathryn L.  
APPLICANT: Thompson, Jeffrey S.  
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND  
TITLE OF INVENTION: PLATELET ACTIVATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue - 29th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/623,611  
FILING DATE: 19901207  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600  
TELEFAX: (212) 715-0674  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-623-611-5

Query Match 90.1%; Score 390; DB 1; Length 99;  
Best Local Similarity 88.9%; Pred. No. 2.7e-29;  
Matches 64; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EAGECCDCCGAPANPCDDATCKLRPQAQCAAGLCCDQCFMKKEGTTCRRARGGDDMDYCN 60  
Db 28 EAGECCDCCGSPANPCDDATCKLRPQAQCAAGLCCDQCFMKKEGTTCRRARGGDDVDYCN 87  
QY 61 GISAGCPRNPFH 72  
Db 88 GISAGCPRNPFH 99

RESULT 15  
US-07-623-611-8  
Sequence 8, Application US/07623611  
Patent No. 5242810  
GENERAL INFORMATION:  
APPLICANT: Maraganore, John M.  
APPLICANT: Chao, Betty H.  
APPLICANT: Strauch, Kathryn L.  
APPLICANT: Thompson, Jeffrey S.  
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND  
TITLE OF INVENTION: PLATELET ACTIVATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue - 29th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/623,611  
FILING DATE: 19901207  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600  
TELEFAX: (212) 715-0674  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-623-611-8

Query Match 90.1%; Score 390; DB 1; Length 99;  
Best Local Similarity 88.9%; Pred. No. 2.7e-29;  
Matches: 64; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY	1	EAGEECDCGADANPCCDATCKLRPGACAGELCCDCCREYKEGTICRMARGDDMDYCN	60
DB	4	EAGEECDCGSPENPCDDATCKLRPGACAGELCCDCCREYKEGTICRMARGDDMDYCN	63
QY	61	GISAGCPRRPFH 72	
DB	64	GISAGCPRRPFH 75	

Search completed: December 3, 2004, 21:40:19  
Job time : 54 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 21:38:18 (Search time 104 Seconds

(Without alignments)  
250.322 Million cell updates/sec

Title: US-10-089-473A-1

Perfect score: 433

Sequence: 1 EAGEEDCDGAPNPPCCDAAT.....DMDDYNGISAGCPNPFHA 73

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	91.2	73	US-09-776-268A-1	Sequence 1, Appl1
2	392.5	90.6	71	US-09-832-501-37	Sequence 37, Appl1
3	392.5	90.6	71	US-10-439-532-7	Sequence 7, Appl1
4	392.5	90.6	71	US-10-712-584-7	Sequence 7, Appl1
5	391	90.3	73	US-09-813-484-15	Sequence 15, Appl1
6	391	90.3	73	US-10-439-532-9	Sequence 9, Appl1
7	391	90.3	73	US-10-712-584-9	Sequence 9, Appl1
8	386	89.1	73	US-10-461-801-15	Sequence 15, Appl1
9	386	89.1	552	US-10-439-532-8	Sequence 8, Appl1
10	386	89.1	552	US-10-712-584-8	Sequence 8, Appl1
11	368	85.0	483	US-10-439-532-2	Sequence 2, Appl1
12	368	85.0	483	US-10-712-584-2	Sequence 2, Appl1
13	360	83.1	478	US-10-078-866-2	Sequence 2, Appl1

14	335	77.4	463	15	US-10-383-588A-2	Sequence 2, Appl1
15	335	77.4	481	15	US-10-383-588A-8	Sequence 8, Appl1
16	333	76.9	73	14	US-10-439-532-10	Sequence 10, Appl1
17	333	76.9	73	16	US-10-712-584-10	Sequence 10, Appl1
18	326	75.3	71	15	US-10-383-588A-6	Sequence 6, Appl1
19	316	73.0	69	9	US-09-813-484-14	Sequence 9, Appl1
20	313	72.3	70	10	US-09-961-856-9	Sequence 10, Appl1
21	312.5	72.2	68	9	US-09-813-484-16	Sequence 16, Appl1
22	312.5	72.2	68	14	US-10-046-801-16	Sequence 16, Appl1
23	305	70.4	70	9	US-09-813-484-17	Sequence 17, Appl1
24	305	70.4	70	14	US-10-046-801-17	Sequence 17, Appl1
25	301	69.5	69	14	US-10-439-532-11	Sequence 14, Appl1
26	287	66.3	68	14	US-10-439-532-11	Sequence 11, Appl1
27	287	66.3	68	16	US-10-712-584-11	Sequence 11, Appl1
28	281	64.9	478	14	US-10-439-532-14	Sequence 14, Appl1
29	281	64.9	478	16	US-10-712-584-14	Sequence 14, Appl1
30	279	64.4	400	9	US-09-921-823-2	Sequence 2, Appl1
31	275	63.5	611	9	US-09-921-823-17	Sequence 17, Appl1
32	260	60.0	111	9	US-09-921-823-23	Sequence 23, Appl1
33	260	60.0	195	9	US-09-921-823-8	Sequence 8, Appl1
34	258.5	59.7	76	10	US-09-877-843-8	Sequence 8, Appl1
35	240.5	55.5	606	14	US-10-439-532-12	Sequence 12, Appl1
36	240.5	55.5	606	16	US-10-712-584-12	Sequence 12, Appl1
37	237	54.7	571	14	US-10-439-532-13	Sequence 13, Appl1
38	237	54.7	571	16	US-10-712-584-13	Sequence 13, Appl1
39	225	52.0	776	9	US-09-908-193-13	Sequence 33, Appl1
40	224	51.7	87	9	US-09-955-504-24	Sequence 24, Appl1
41	224	51.7	87	13	US-10-125-452-24	Sequence 24, Appl1
42	224	51.7	150	9	US-09-983-531A-18	Sequence 16, Appl1
43	224	51.7	394	9	US-09-983-531A-16	Sequence 16, Appl1
44	224	51.7	395	15	US-10-343-251A-45	Sequence 45, Appl1
45	224	51.7	427	9	US-09-983-531A-20	Sequence 20, Appl1

## ALIGNMENTS

RESULT 1

US-09-776-268A-1

Sequence 1, Application US/09776268A

Publication No. US2001002342A1

GENERAL INFORMATION:

APPLICANT: KIM, DOO-SIK

APPLICANT: CHUNG, Kwang Hoe

APPLICANT: KANG, In-Cheol

TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT

FILE REFERENCE: 0136/16733-US1

CURRENT APPLICATION NUMBER: US/09/776, 268A

PRIOR FILING DATE: 2002-02-02

PRIOR APPLICATION NUMBER: US 09/335, 088

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: KR 99-20579

PRIOR FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: KR 98-23778

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 73

TYPE: PRT

ORGANISM: Agkistrodon halys brevicaudus

US-09-776-268A-1

Query Match 91.2%; Score 395; DB 9; Length 73;

Best Local Similarity 90.4%; Pred. No. 3,5e-31;

Matches 66; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEEDCDGAPNPPCCDAATCKLRGAGCAEGICDQCFMKEGTCRMAEGDDMDYDYN 60

DB 1 EAGEEDCDGAPNPPCCDAATCKLRGAGCAEGICDQCFMKEGTCRMAEGDDMDYDYN 60

QY 61 GISAGCPNPFHA 73

|||||

Db 61 GISAGCPRNPFH 73

RESULT 2  
US-09-832-501-37  
Sequence 37, Application US/09832501  
Publication No. US2003019043A1  
GENERAL INFORMATION:  
APPLICANT: Ballance, David J.  
APPLICANT: Sleep, Darrell  
APPLICANT: Turner, Andrew J.  
APPLICANT: Sadeghi, Homa  
APPLICANT: Prior, Christopher P.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PFS42  
CURRENT APPLICATION NUMBER: US/09/832,501  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/229,358  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: 60/256,931  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/199,384  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 37  
LENGTH: 71  
TYPE: PRT  
ORGANISM: Agkistrodon piscivorus  
US-09-832-501-37

Query Match 90.6%; Score 392.5; DB 10; Length 71;  
Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;  
Matches 65; Conservative 5; Mismatches 1;

QY 1 EAGEECDCGAPANPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICRMARGDDMDYCN 60  
1 EAGEECDCGSPENPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

Db 61 GISAGCPRNPFH 72  
60 GISAGCPRNPFH 71

RESULT 3  
US-10-439-532-7  
Sequence 7, Application US/10439532  
Publication No. US20030186884A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST  
TITLE OF INVENTION: OTHER CONDITIONS  
FILE REFERENCE: 1279-338N2/09801388  
CURRENT APPLICATION NUMBER: US/10/439,532  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 7  
LENGTH: 71  
TYPE: PRT  
ORGANISM: Agkistrodon piscivorus  
US-10-439-532-7

Query Match 90.6%; Score 392.5; DB 14; Length 71;  
Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;  
Matches 65; Conservative 5; Mismatches 1;

QY 1 EAGEECDCGAPANPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICRMARGDDMDYCN 60  
1 EAGEECDCGSPENPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

QY 61 GISAGCPRNPFH 72  
Db 60 GISAGCPRNPFH 71

RESULT 4  
US-10-712-584-7  
Sequence 7, Application US/10712584  
Publication No. US20040132659A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
APPLICANT: Markland, Francis S.  
APPLICANT: Rittner, Matthew  
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS  
TITLE OF INVENTION: OTHER CONDITIONS  
FILE REFERENCE: 1279-338N3/09801388  
CURRENT APPLICATION NUMBER: US/10/712,584  
CURRENT FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
PRIOR APPLICATION NUMBER: US 08/141,321  
PRIOR FILING DATE: 1993-10-22  
PRIOR APPLICATION NUMBER: US 08/540,423  
PRIOR FILING DATE: 1995-10-10  
PRIOR APPLICATION NUMBER: US 08/632,691  
PRIOR FILING DATE: 1996-04-15  
PRIOR APPLICATION NUMBER: US 08/745,603  
PRIOR FILING DATE: 1996-11-08  
PRIOR APPLICATION NUMBER: US 09/163,047  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: US09/460,295  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 7  
LENGTH: 71  
TYPE: PRT  
ORGANISM: Agkistrodon piscivorus  
US-10-712-584-7

Query Match 90.6%; Score 392.5; DB 16; Length 71;  
Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;  
Matches 65; Conservative 5; Mismatches 1;

QY 1 EAGEECDCGAPANPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICRMARGDDMDYCN 60  
1 EAGEECDCGSPENPCDDATCTLRFGAQCAGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

Db 61 GISAGCPRNPFH 72  
60 GISAGCPRNPFH 71

RESULT 5  
US-09-813-484-15  
Sequence 15, Application US/09813484  
Publication No. US20010031243A1  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C.  
TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseou  
TITLE OF INVENTION: Filled Compositions  
FILE REFERENCE: UNGR1600  
CURRENT APPLICATION NUMBER: US/09/813,484  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 08/925,847  
PRIOR FILING DATE: 1997-09-15  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 15  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:



FILE OF INVENTION: CONJUGATION (CN)  
 TITLE OF INVENTION: OTHER CONDITIONS  
 FILE REFERENCE: 1279-338N2/09801388  
 CURRENT APPLICATION NUMBER: US/10/439,532  
 CURRENT FILING DATE: 2003-05-16

PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 552  
TYPE: PR  
ORGANISM: Trimeresurus gramineus  
US-10-439-532-8

Query Match 89.1%; Score 386; DB 14; Length 552;  
Best Local Similarity 84.9%; Pred. No. 1.5e-29;  
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 480 EAGEBCDGCSPANPCDDATCTLRPGACAGELCCDCCSFIIEGTICRIARGDDLDYCN 539

QY 61 GISACCPNPFHA 73  
DB 540 GRSACCPNPFHA 552

RESULT 10  
US-10-712-584-8  
Sequence 8, Application US/10712584  
Publication No. US20040132659A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
APPLICANT: Markland, Francis S.  
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST  
TITLE OF INVENTION: OTHER CONDITIONS  
FILE REFERENCE: 1279-338N3/09801388  
CURRENT APPLICATION NUMBER: US/10/712,584  
PRIOR FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
PRIOR APPLICATION NUMBER: US 08/141,321  
PRIOR FILING DATE: 1993-10-22  
PRIOR APPLICATION NUMBER: US 08/540,423  
PRIOR FILING DATE: 1995-10-10  
PRIOR APPLICATION NUMBER: US 08/632,691  
PRIOR FILING DATE: 1996-04-15  
PRIOR APPLICATION NUMBER: US 08/745,603  
PRIOR FILING DATE: 1996-11-08  
PRIOR APPLICATION NUMBER: US 09/163,047  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: US09/460,295  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 552  
TYPE: PR  
ORGANISM: Trimeresurus gramineus  
US-10-712-584-8

Query Match 89.1%; Score 386; DB 16; Length 552;  
Best Local Similarity 84.9%; Pred. No. 1.5e-29;  
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 480 EAGEBCDGCSPANPCDDATCTLRPGACAGELCCDCCSFIIEGTICRIARGDDLDYCN 539  
QY 61 GISACCPNPFHA 73  
DB 540 GRSACCPNPFHA 552

RESULT 11  
US-10-439-532-2

Sequence 2, Application US/10439532  
Publication No. US20030186884A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
APPLICANT: Markland, Francis S.  
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS  
TITLE OF INVENTION: OTHER CONDITIONS  
FILE REFERENCE: 1279-338N2/09801388  
CURRENT APPLICATION NUMBER: US/10/439,532  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 483  
TYPE: PR  
ORGANISM: Agkistrodon contortrix  
US-10-439-532-2

Query Match 85.0%; Score 368; DB 14; Length 483;  
Best Local Similarity 83.6%; Pred. No. 7.4e-28;  
Matches 61; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 411 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCSFIIEGTICRIARGDDLDYCN 470  
QY 61 GISACCPNPFHA 73  
DB 471 GISACCPNPFHA 483

RESULT 12  
US-10-712-584-2  
Sequence 2, Application US/10712584  
Publication No. US20040132659A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
APPLICANT: Markland, Francis S.  
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS  
TITLE OF INVENTION: OTHER CONDITIONS  
FILE REFERENCE: 1279-338N3/09801388  
CURRENT APPLICATION NUMBER: US/10/712,584  
CURRENT FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
PRIOR APPLICATION NUMBER: US 08/141,321  
PRIOR FILING DATE: 1993-10-22  
PRIOR APPLICATION NUMBER: US 08/540,423  
PRIOR FILING DATE: 1995-10-10  
PRIOR APPLICATION NUMBER: US 08/632,691  
PRIOR FILING DATE: 1996-04-15  
PRIOR APPLICATION NUMBER: US 08/745,603  
PRIOR FILING DATE: 1996-11-08  
PRIOR APPLICATION NUMBER: US 09/163,047  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: US09/460,295  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 483  
TYPE: PR  
ORGANISM: Agkistrodon contortrix  
US-10-712-584-2

Query Match 85.0%; Score 368; DB 16; Length 483;  
Best Local Similarity 83.6%; Pred. No. 7.4e-28;  
Matches 61; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMARGDDMDYCN 60  
DB 411 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCSFIIEGTICRIARGDDLDYCN 470

Db 411 ETGESEDPDAPANPCDAATCKLTGSGCAGLCCDQCKFMKEGTVCRARAGDDLDYCN 470  
QY 61 GISAGCPNPFHA 73  
Db 471 GISAGCPNPFHA 483

RESULT 13  
US-10-078-866-2  
; Sequence 2, Application US/1007866  
; Publication No. US2003096393A1  
; GENERAL INFORMATION:  
; APPLICANT: FOX, BRIAN A  
; APPLICANT: SHEPPARD, PAUL O.  
; TITLE OF INVENTION: Disintegrin Homolog, zsnk16  
; FILE REFERENCE: 01-05  
; CURRENT APPLICATION NUMBER: US/10/078,866  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/270,276  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: *Sistrurus miliarius*  
US-10-078-866-2

Query Match 83.1%; Score 360; DB 14; Length 478;  
Best Local Similarity 83.6%; Pred. No. 4,4e-27;  
Matches 61; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 60  
Db 406 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 465  
QY 61 GISAGCPNPFHA 73  
Db 466 GOSADCPNPFHA 478

RESULT 14  
US-10-383-588A-2  
; Sequence 2, Application US/10383588A  
; Publication No. US20040091887A1  
; GENERAL INFORMATION:  
; APPLICANT: GUO, Yaw-Wen  
; APPLICANT: HO, Pei-Hsiun  
; TITLE OF INVENTION: Mucroslyin and Its Gene  
; FILE REFERENCE: 87146043-2001  
; CURRENT APPLICATION NUMBER: US/10/383,588A  
; CURRENT FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: *Trimeresurus mucrosquamatus*  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(463)  
US-10-383-588A-2

Query Match 77.4%; Score 335; DB 15; Length 463;  
Best Local Similarity 82.6%; Pred. No. 1.2e-24;  
Matches 57; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 60  
Db 391 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 450  
QY 61 GISAGCPN 69

Db 451 GOSADCPN 459

RESULT 15  
US-10-383-588A-8  
; Sequence 8, Application US/10383588A  
; Publication No. US20040091887A1  
; GENERAL INFORMATION:  
; APPLICANT: GUO, Yaw-Wen  
; APPLICANT: HO, Pei-Hsiun  
; TITLE OF INVENTION: Mucroslyin and Its Gene  
; FILE REFERENCE: 87146043-2001  
; CURRENT APPLICATION NUMBER: US/10/383,588A  
; CURRENT FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: *Trimeresurus mucrosquamatus*  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(481)  
US-10-383-588A-8

Query Match 77.4%; Score 335; DB 15; Length 481;  
Best Local Similarity 82.6%; Pred. No. 1.2e-24;  
Matches 57; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 60  
Db 409 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDQCFMKEGTCRMARGDMDYCN 468  
QY 61 GISAGCPN 69  
Db 469 GOSADCPN 477

Search completed: December 3, 2004, 21:49:16  
Job time : 105 secs

**This Page Blank (uspio)**